

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 28, 2005, 13:43:04 ; Search time 147.538 Seconds  
(without alignments)  
375.236 Million cell updates/sec

Title: US-09-920-137F-7  
Perfect score: 668  
Sequence: 1 QVQLVESGGGVQPGKSLRL.....NYYYYGMDVMWGQGTITVTVSS 126

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_21:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	657.5	98.4	146	5 AAM51171	Aam51171 Human rec
2	652.5	97.7	146	5 AAM51170	Aam51170 Human rec
3	627.5	93.9	146	5 AAM51169	Aam51169 Human rec
4	620.5	92.9	146	5 AAM51172	Aam51172 Human rec
5	615.5	92.1	146	5 AAM51168	Aam51168 Human rec
6	583	87.3	135	7 ADD28320	Add28320 Human het
7	583	87.3	135	7 ADD28236	Add28236 Human het
8	583	87.3	135	9 ADV86823	Adv86823 Bacillus
9	582	87.1	124	6 ADA89238	Ada89238 Human ant
10	581.5	87.1	127	2 AAY17954	Aay17954 Human D4
11	581.5	87.1	138	2 AAW80815	Aaw80815 Amino aci
12	581.5	87.1	457	9 AEC16143	Aec16143 Human ant
13	581.5	87.1	523	3 AAY44994	Aay44994 HD70scFv-
14	581.5	87.1	524	3 AAY44995	Aay44995 HD70scFv-
15	581	87.0	126	7 ADK18593	Adk18593 Anti-huma
16	581	87.0	126	7 ADK18785	Adk18785 Anti-huma
17	581	87.0	126	7 ADK18858	Adk18858 Anti-huma
18	581	87.0	126	8 ADL25404	Adl25404 Human mAb
19	579	86.7	126	7 ADK18786	Adk18786 Anti-huma
20	579	86.7	126	7 ADK18822	Adk18822 Anti-huma
21	579	86.7	126	7 ADK18882	Adk18882 Anti-huma
22	579	86.7	126	7 ADK18601	Adk18601 Anti-huma
23	579	86.7	126	8 ADL25420	Adl25420 Human mAb
24	579	86.7	126	8 ADP22222	Adp22222 Human ant

25	577.5	86.5	125	8 ADP22316	Adp22316 Human ant
26	577	86.4	115	5 AAM51164	Aam51164 Anti-tumo
27	577	86.4	141	9 ADV67314	Adv67314 Amino aci
28	576	86.2	118	5 AAM51167	Aam51167 Human DP-
29	575.5	86.2	125	8 ADP22300	Adp22300 Human ant
30	575.5	86.2	125	8 ADP22312	Adp22312 Human ant
31	573	85.8	134	8 ADP22348	Adp22348 Human ant
32	572.5	85.7	252	5 ABP45720	Abp45720 Human Bly
33	572.5	85.7	252	7 ADG96547	Adg96547 Single ch
34	572.5	85.7	451	3 AAY93734	Aay93734 The heavy
35	572.5	85.7	451	6 AAE35889	Aae35889 Human 11.
36	572	85.6	122	8 ADP22128	Adp22128 Human ant
37	572	85.6	126	7 ADK18821	Adk18821 Anti-huma
38	571.5	85.6	123	8 ADS84372	Ads84372 Human ant
39	571.5	85.6	123	8 ADR68514	Adr68514 Anti-EPO-
40	571	85.5	135	7 ADD28317	Add28317 Human het
41	570.5	85.4	125	7 ADE28451	Ade28451 Human ant
42	570.5	85.4	127	9 AEB27731	Aeb27731 Prostate
43	570.5	85.4	252	9 AEB27751	Aeb27751 Anti-pros
44	570.5	85.4	470	7 ADE28475	Ade28475 Human ant
45	569.5	85.3	122	9 AEB45960	Aeb45960 Human mon

ALIGNMENTS

RESULT 1  
AAM51171  
ID AAM51171 standard; protein; 146 AA.  
XX  
AC AAM51171;

DT 10-JUN-2002 (first entry)  
XX

DE Human recombinant mAb TNV148(B) heavy chain variable region.  
XX

KW Tumour necrosis factor alpha; TNF; antibody; heavy chain; CDR;  
KW complementarity determining region; antirheumatic; antiarthritic;  
KW antiulcer; antiasthmatic; antiallergic; antiinflammatory; antisickling;  
KW antidiabetic; antiarteriosclerotic; antiatherosclerotic; vasotrophic;  
KW antiangular; cardiant; antibacterial; virucide; fungicide; antileprotic;  
KW protozoacide; cytostatic; neuroprotective; antiparkinsonian; nootropic;  
KW human; diagnosis; therapy; TNV148; monoclonal antibody; mAb.

OS Homo sapiens.  
OS Synthetic.

Key	Location/Qualifiers
Peptide	1. .19
	/label= Signal_peptide
	/note= "amino acids 1-7 are PCR primer-encoded and may differ from the native sequence"
Protein	20. .146
	/label= Mature_protein
Region	31. .49
	/label= FR1
Region	50. .54
	/label= CDR1
Region	55. .68
	/label= FR2
Region	69. .85
	/label= CDR2
Region	86. .117
	/label= FR3
Misc-difference	94
	/note= "wild-type Pro substituted by Ser"
Region	118. .135
	/label= CDR3
Misc-difference	126
	/note= "encoded by A"
Region	136. .146
	/label= J6

PN WO200212502-A2.  
XX 14-FEB-2002.  
PD 07-AUG-2001; 2001WO-US024785.  
XX 07-AUG-2000; 2000US-0223360P.  
PF 29-SEP-2000; 2000US-0236826P.  
PR 01-AUG-2001; 2001US-00920137.  
XX (CENZ ) CENTOCOR INC.  
PA Giles-Komar J, Knight DM, Heavner G, Scallion B, Shealy D;  
XX WPI; 2002-217194/27.  
XX N-PSDB; ABL53511.  
DR Novel isolated mammalian anti-tumor necrosis factor antibody, useful for  
PT treating sickle cell anemia, diabetes, atherosclerosis, restenosis,  
PT angina pectoris, myocardial infarction, leprosy.  
XX Example 3; Fig 4; 131pp; English.  
XX The present sequence is that of the heavy chain variable region of anti-  
CC tumour necrosis factor (TNF) human recombinant monoclonal antibody (mAb)  
CC TNV148(B). TNV148(B) was produced by site-directed mutagenesis of TNV148  
CC (see AAM51170), replacing residue Pro-94 with a germline Ser. TNV148 was  
CC 1 of 8 human mAbs produced from a GentNV fusion using spleen cells from a  
CC hybrid mouse containing human variable and constant region antibody  
CC transgenes that was immunised with human TNF alpha. The human mAbs bound  
CC immobilised human TNF alpha with high avidity and had a totally human  
CC IgG1, kappa isotype. They showed relatedness to each other and to the  
CC human germline DP-46 heavy chain sequence (see AAM51167). The invention  
CC provides isolated human, primate, rodent, mammalian, chimeric, humanised  
CC and/or complementarity determining region (CDR)-grafted anti-TNF  
CC antibodies, immunoglobulins, cleavage products and other specified  
CC portions and variants, as well as anti-TNF antibody compositions,  
CC encoding or complementary nucleic acids, vectors, host cells,  
CC compositions, formulations, devices, transgenic animals, transgenic  
CC plants, and methods of making and using them. The anti-TNF antibody  
CC comprises at least a portion of an immunoglobulin molecule, especially  
CC the heavy chain and/or light chain variable regions given in the present  
CC sequence and in AAM51165, or either all of the CDRs of the heavy chain  
CC (see AAM51158-60) or all of the CDRs of the light chain (see AAM51161-  
CC 63). The antibodies may inhibit TNF-induced cell adhesion molecules,  
CC inhibit TNF binding to receptor, or provide Arthritic Index improvement  
CC in a mouse model. They are useful for diagnosing or treating a TNF  
CC related condition in a cell, tissue, organ or animal (claimed) such as  
CC rheumatoid arthritis, gastric ulcer, asthma, allergic rhinitis, Crohn's  
CC pathology, sickle cell anaemia, diabetes, a cardiovascular disease such  
CC as arteriosclerosis, atherosclerosis, restenosis, angina pectoris or  
CC myocardial infarction, an infectious disease in a cell such as bacterial,  
CC viral, and fungal infections, pneumonia, leprosy and malaria, a malignant  
CC disease such as leukaemia, chronic myelocytic leukaemia, Burkitt's  
CC lymphoma and multiple myeloma, or a neurological disease such as multiple  
CC sclerosis, Parkinson's disease, spinal ataxia, Alzheimer's disease and  
CC Creutzfeldt-Jakob disease. TNV148(B) may be especially useful as an  
XX antiinflammatory  
SQ Sequence 146 AA;  
  
Query Match 98.4%; Score 657.5; DB 5; Length 146;  
Best Local Similarity 99.2%; Pred. No. 7.3e-49;  
Matches 126; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
  
QY 1 QVQLVSGGWWQPGRSRLRLSCAASGFIFSSYAMHWVRQAPGNGLEWVAFMSYDGSNKKY 60  
DB |||||  
20 QVQLVSGGWWQPGRSRLRLSCAASGFIFSSYAMHWVRQAPGNGLEWVAFMSYDGSNKKY 79  
  
QY 61 ADSVKGRFTISRDN SKNTLLYQMNSLRAEDTAVYYCARDRGIAAGGN-YYYYGMDVWGQG 119  
DB |||||  
80 ADSVKGRFTISRDN SKNTLLYQMNSLRAEDTAVYYCARDRGIAAGGNYYYYGMDVWGQG 139

QY 120 TTVTVSS 126  
Db |||||  
140 TTVTVSS 146  
  
RESULT 2  
AAM51170  
ID AAM51170 standard; protein; 146 AA.  
XX  
AC AAM51170;  
XX  
DT 10-JUN-2002 (first entry)  
XX  
DE Human recombinant mAb TNV148 heavy chain variable region.  
XX  
KW Tumour necrosis factor alpha; TNF; antibody; heavy chain; CDR;  
KW complementarity determining region; antirheumatic; antiarthritic;  
KW antiulcer; antiasthmatic; antiallergic; antiinflammatory; antisickling;  
KW antidiabetic; antiarteriosclerotic; antiatherosclerotic; vasotropic;  
KW antianginal; cardiant; antibacterial; virucide; fungicide; antileprotic;  
KW protozoacide; cytostatic; neuroprotective; antiparkinsonian; nootropic;  
KW human; diagnosis; therapy; TNV148; monoclonal antibody; mAb.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1. .19 /label= Signal\_peptide  
FT /note= "amino acids 1-7 are PCR primer-encoded and may  
FT differ from the native sequence"  
FT Protein 20. .146 /label= Mature\_protein  
FT Region 31. .49 /label= FR1  
FT Region 50. .54 /label= CDR1  
FT Region 55. .68 /label= FR2  
FT Region 69. .85 /label= CDR2  
FT Region 86. .117 /label= FR3  
FT Region 118. .135 /label= CDR3  
FT Misc-difference 126 /note= "encoded by A"  
FT Region 136. .146 /label= J6  
XX  
PN WO200212502-A2.  
XX 14-FEB-2002.  
XX 07-AUG-2001; 2001WO-US024785.  
XX 07-AUG-2000; 2000US-0223360P.  
PR 29-SEP-2000; 2000US-0236826P.  
PR 01-AUG-2001; 2001US-00920137.  
XX (CENZ ) CENTOCOR INC.  
PA Giles-Komar J, Knight DM, Heavner G, Scallion B, Shealy D;  
XX WPI; 2002-217194/27.  
XX N-PSDB; ABL53510.  
XX Novel isolated mammalian anti-tumor necrosis factor antibody, useful for  
PT treating sickle cell anemia, diabetes, atherosclerosis, restenosis,  
PT angina pectoris, myocardial infarction, leprosy.  
XX Example 3; Fig 4; 131pp; English.  
XX The present sequence is that of the heavy chain variable region of anti-

CC tumour necrosis factor (TNF) human recombinant monoclonal antibody (mAb)  
CC TNV148. TNV148 was 1 of 8 human mAbs produced from a GentNV fusion using  
CC spleen cells from a hybrid mouse containing human variable and constant  
CC region antibody transgenes that was immunised with human TNF alpha. The  
CC human mAbs bound immobilised human TNF alpha with high avidity and had a  
CC totally human IgG1, kappa isotype. They showed relatedness to each other  
CC and to the human germline DP-46 heavy chain sequence (see AAM51167). The  
CC invention provides isolated human, primate, rodent, mammalian, chimeric,  
CC humanised and/or complementarity determining region (CDR)-grafted anti-  
CC TNF antibodies, immunoglobulins, cleavage products and other specified  
CC portions and variants, as well as anti-TNF antibody compositions,  
CC encoding or complementary nucleic acids, vectors, host cells,  
CC compositions, formulations, devices, transgenic animals, transgenic  
CC plants, and methods of making and using them. The anti-TNF antibody  
CC comprises at least a portion of an immunoglobulin molecule, especially  
CC the heavy chain and/or light chain variable regions given in the present  
CC sequence and in AAM51165, or either all of the CDRs of the heavy chain  
CC (see AAM51158-60) or all of the CDRs of the light chain (see AAM51161-  
CC 63). The antibodies may inhibit TNF-induced cell adhesion molecules,  
CC inhibit TNF binding to receptor, or provide Arthritic Index improvement  
CC in a mouse model. They are useful for diagnosing or treating a TNF  
CC related condition in a cell, tissue, organ or animal (claimed) such as  
CC rheumatoid arthritis, gastric ulcer, asthma, allergic rhinitis, Crohn's  
CC pathology, sickle cell anaemia, diabetes, a cardiovascular disease such  
CC as arteriosclerosis, atherosclerosis, restenosis, angina pectoris or  
CC myocardial infarction, an infectious disease in a cell such as bacterial,  
CC viral, and fungal infections, pneumonia, leprosy and malaria, a malignant  
CC disease such as leukaemia, chronic myelocytic leukaemia, Burkitt's  
CC lymphoma and multiple myeloma, or a neurological disease such as multiple  
CC sclerosis, Parkinson's disease, spinal ataxia, Alzheimer's disease and  
CC Creutzfeldt-Jakob disease. TNV148 may be especially useful as an  
CC antiinflammatory  
XX  
SQ Sequence 146 AA;

Query Match 97.7%; Score 652.5; DB 5; Length 146;  
Best Local Similarity 98.4%; Pred. No. 2e-48;  
Matches 125; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 QVQLVSGGTVQPGRLSLRSCAASGFIFSSYAMHWVRQAPGNGLEWVAFMSYDGSNKKY 60  
Db |||||  
20 QVQLVSGGTVQPGRLSLRSCAASGFIFSSYAMHWVRQAPGNGLEWVAFMSYDGSNKKY 79  
QY 61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDRGIAAGGN-YYYYGMDVWGQG 119  
Db |||||  
80 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDRGIAAGGNYYYYYGMVWGQG 139  
QY 120 TTVTVSS 126  
Db |||||  
140 TTVTVSS 146

RESULT 3  
AAM51169  
ID AAM51169 standard; protein; 146 AA.  
XX  
AC AAM51169;  
XX

DT 10-JUN-2002 (first entry)

XX Human recombinant mAb TNV15 heavy chain variable region.

DE Tumour necrosis factor alpha; TNF; antibody; heavy chain; CDR;  
KW complementarity determining region; antirheumatic; antiarthritic;  
KW antiulcer; antiasthmatic; antiallergic; antiinflammatory; antisickling;  
KW antidiabetic; antiarteriosclerotic; antiatherosclerotic; vasotropic;  
KW antianginal; cardiast; antibacterial; virucide; fungicide; antileprotic;  
KW protozoacide; cytostatic; neuroprotective; antiparkinsonian; nootropic;  
KW human; diagnosis; therapy; TNV15; monoclonal antibody; mAb.

OS Homo sapiens.

XX  
FH Key Location/Qualifiers

FT Peptide  
FT 1. .19  
FT /label= Signal\_peptide  
FT /note= "amino acids 1-7 are PCR primer-encoded and may  
FT differ from the native sequence"  
FT 20. .146  
FT /label= Mature\_protein  
FT 31. .49  
FT /label= FR1  
FT 50. .54  
FT /label= CDR1  
FT 55. .68  
FT /label= FR2  
FT 69. .85  
FT /label= CDR2  
FT 86. .117  
FT /label= FR3  
FT 118. .135  
FT /label= CDR3  
FT Misc-difference 126  
FT /note= "encoded by A"  
FT 136. .146  
FT /label= J6  
FT  
XX WO200212502-A2.  
PN  
XX 14-FEB-2002.  
PD  
XX 07-AUG-2001; 2001WO-US024785.  
XX 07-AUG-2000; 2000US-0223360P.  
PR 29-SEP-2000; 2000US-0236826P.  
PR 01-AUG-2001; 2001US-00920137.  
XX  
PA (CENZ ) CENTOCOR INC.  
XX  
XX Giles-Komar J, Knight DM, Heavner G, Scallion B, Shealy D;  
PI WPI; 2002-217194/27.  
XX N-PSDB; ABL53509.  
DR  
DR Novel isolated mammalian anti-tumor necrosis factor antibody, useful for  
PT treating sickle cell anemia, diabetes, atherosclerosis, restenosis,  
PT angina pectoris, myocardial infarction, leprosy.  
XX  
PS Example 3; Fig 4; 131pp; English.  
XX  
CC The present sequence is that of the heavy chain variable region of anti-  
CC tumour necrosis factor (TNF) human recombinant monoclonal antibody (mAb)  
CC TNV15. TNV15 was 1 of 8 human mAbs produced from a GentNV fusion using  
CC spleen cells from a hybrid mouse containing human variable and constant  
CC region antibody transgenes that was immunised with human TNF alpha. The  
CC human mAbs bound immobilised human TNF alpha with high avidity and had a  
CC totally human IgG1, kappa isotype. They showed relatedness to each other  
CC and to the human germline DP-46 heavy chain sequence (see AAM51167). The  
CC invention provides isolated human, primate, rodent, mammalian, chimeric,  
CC humanised and/or complementarity determining region (CDR)-grafted anti-  
CC TNF antibodies, immunoglobulins, cleavage products and other specified  
CC portions and variants, as well as anti-TNF antibody compositions,  
CC encoding or complementary nucleic acids, vectors, host cells,  
CC compositions, formulations, devices, transgenic animals, transgenic  
CC plants, and methods of making and using them. The anti-TNF antibody  
CC comprises at least a portion of an immunoglobulin molecule, especially  
CC the heavy chain and/or light chain variable regions given in the present  
CC sequence and in AAM51165, or either all of the CDRs of the heavy chain  
CC (see AAM51158-60) or all of the CDRs of the light chain (see AAM51161-  
CC 63). The antibodies may inhibit TNF-induced cell adhesion molecules,  
CC inhibit TNF binding to receptor, or provide Arthritic Index improvement  
CC in a mouse model. They are useful for diagnosing or treating a TNF  
CC related condition in a cell, tissue, organ or animal (claimed) such as  
CC rheumatoid arthritis, gastric ulcer, asthma, allergic rhinitis, Crohn's  
CC pathology, sickle cell anaemia, diabetes, a cardiovascular disease such  
CC as arteriosclerosis, atherosclerosis, restenosis, angina pectoris or  
CC myocardial infarction, an infectious disease in a cell such as bacterial,  
CC

CC viral, and fungal infections, pneumonia, leprosy and malaria, a malignant  
CC disease such as leukaemia, chronic myelocytic leukaemia, Burkitt's  
CC lymphoma and multiple myeloma, or a neurological disease such as multiple  
CC sclerosis, Parkinson's disease, spinal ataxia, Alzheimer's disease and  
CC Creutzfeldt-Jakob disease  
XX  
SQ Sequence 146 AA;

Query Match 93.9%; Score 627.5; DB 5; Length 146;  
Best Local Similarity 93.7%; Pred. No. 2.8e-46;  
Matches 119; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

QY 1 QVQLVESGGGVQPGRSRLRLSCAASGFIFSSYAMHWVRQAPGNGLEWVAFMSYDGSNKKY 60  
Db 20 QVQLVESGGGVQPGRSRLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAFILYDGSNKKY 79  
QY 61 ADSVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCARDRGIAAGN-YYYYGMDVWGQG 119  
Db 80 ADSVKGRFTISRDN SKNALYLQMN SLRAEDTAVYYCARDRGVSAGNYYYYYGMVDVWGQG 139  
QY 120 TTVTVSS 126  
Db 140 TTVTVSS 146

RESULT 4  
AAM51172  
ID AAM51172 standard; protein; 146 AA.  
XX  
AC AAM51172;  
DT 10-JUN-2002 (first entry)  
XX  
DE Human recombinant mAb TNV196 heavy chain variable region.

XX  
KW Tumour necrosis factor alpha; TNF; antibody; heavy chain; CDR;  
KW complementarity determining region; antirheumatic; antiarthritic;  
KW antiulcer; antiasthmatic; antiallergic; antiinflammatory; antisickling;  
KW antidiabetic; antiarteriosclerotic; antiatherosclerotic; vasotropic;  
KW antiangular; cardiant; antibacterial; virucide; fungicide; antileprotic;  
KW protozoacide; cytostatic; neuroprotective; antiparkinsonian; nootropic;  
KW human; diagnosis; therapy; TNV196; monoclonal antibody; mAb.

XX Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1. .19 /label= Signal\_peptide  
FT /note= "amino acids 1-7 are PCR primer-encoded and may  
FT differ from the native sequence"  
FT Protein 20. .146  
FT /label= Mature\_protein  
FT Region 31. .49  
FT /label= FR1  
FT Region 50. .54  
FT /label= CDR1  
FT Region 55. .68  
FT /label= FR2  
FT Region 69. .85  
FT /label= CDR2  
FT Region 86. .117  
FT /label= FR3  
FT Region 118. .135  
FT /label= CDR3  
FT Misc-difference 126 /note= "encoded by A"  
FT Region 136. .146  
FT /label= J6

XX  
PN WO200212502-A2.  
XX  
PD 14-FEB-2002.  
XX

PF 07-AUG-2001; 2001WO-US024785.  
XX  
PR 07-AUG-2000; 2000US-0223360P.  
PR 29-SEP-2000; 2000US-0236826P.  
PR 01-AUG-2001; 2001US-00920137.  
XX  
PA (CENZ ) CENTOCOR INC.  
XX  
PI Giles-Komar J, Knight DM, Heavner G, Scallan B, Shealy D;  
XX  
DR WPI; 2002-217194/27.  
DR N-PSDB; ABL53512.

XX Novel isolated mammalian anti-tumor necrosis factor antibody, useful for  
PT treating sickle cell anemia, diabetes, atherosclerosis, restenosis,  
PT angina pectoris, myocardial infarction, leprosy.  
XX  
PS Example 3; Fig 4; 131pp; English.  
XX

CC The present sequence is that of the heavy chain variable region of anti-  
CC tumour necrosis factor (TNF) human recombinant monoclonal antibody (mAb)  
CC TNV196. TNV196 was 1 of 8 human mAbs produced from a GentNV fusion using  
CC spleen cells from a hybrid mouse containing human variable and constant  
CC region antibody transgenes that was immunised with human TNF alpha. The  
CC human mAbs bound immobilised human TNF alpha with high avidity and had a  
CC totally human IgG1, kappa isotype. They showed relatedness to each other  
CC and to the human germline DP-46 heavy chain sequence (see AAM51167). The  
CC invention provides isolated human, primate, rodent, mammalian, chimeric,  
CC humanised and/or complementarity determining region (CDR)-grafted anti-  
CC TNF antibodies, immunoglobulins, cleavage products and other specified  
CC portions and variants, as well as anti-TNF antibody compositions,  
CC encoding or complementary nucleic acids, vectors, host cells,  
CC compositions, formulations, devices, transgenic animals, transgenic  
CC plants, and methods of making and using them. The anti-TNF antibody  
CC comprises at least a portion of an immunoglobulin molecule, especially  
CC the heavy chain and/or light chain variable regions given in the present  
CC sequence and in AAM51165, or either all of the CDRs of the heavy chain  
CC (see AAM51158-60) or all of the CDRs of the light chain (see AAM51161-  
CC 63). The antibodies may inhibit TNF-induced cell adhesion molecules,  
CC inhibit TNF binding to receptor, or provide Arthritic Index improvement  
CC in a mouse model. They are useful for diagnosing or treating a TNF  
CC related condition in a cell, tissue, organ or animal (claimed) such as  
CC rheumatoid arthritis, gastric ulcer, asthma, allergic rhinitis, Crohn's  
CC pathology, sickle cell anaemia, diabetes, a cardiovascular disease such  
CC as arteriosclerosis, atherosclerosis, restenosis, angina pectoris or  
CC myocardial infarction, an infectious disease in a cell such as bacterial,  
CC viral, and fungal infections, pneumonia, leprosy and malaria, a malignant  
CC disease such as leukaemia, chronic myelocytic leukaemia, Burkitt's  
CC lymphoma and multiple myeloma, or a neurological disease such as multiple  
CC sclerosis, Parkinson's disease, spinal ataxia, Alzheimer's disease and  
CC Creutzfeldt-Jakob disease

XX  
SQ Sequence 146 AA;

Query Match 92.9%; Score 620.5; DB 5; Length 146;  
Best Local Similarity 92.9%; Pred. No. 1.1e-45;  
Matches 118; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY 1 QVQLVESGGGVQPGRSRLRLSCAASGFIFSSYAMHWVRQAPGNGLEWVAFMSYDGSNKKY 60  
Db 20 QVQLVESGGGVQPGRSRLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAFISYDGSNKKS 79  
QY 61 ADSVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCARDRGIAAGN-YYYYGMDVWGQG 119  
Db 80 ADSVKGRFTISRDN SKNTLYLQMN SLRAEDTAVFYCARDRGIGAGNYYYYYGMVDVWGQG 139  
QY 120 TTVTVSS 126  
Db 140 TTVTVSS 146

RESULT 5  
AAM51168



ID AAM51168 standard; protein; 146 AA.  
AC AAM51168;  
XX  
DT 10-JUN-2002 (first entry)  
XX  
DE Human recombinant mAb TNV14 heavy chain variable region.  
XX  
KW Tumour necrosis factor alpha; TNF; antibody; heavy chain; CDR;  
KW complementarity determining region; antiarthritis;  
KW antilucer; antiasthmatic; antiallergic; antiinflammatory; antisickling;  
KW antidiabetic; antiarteriosclerotic; antiatherosclerotic; vasotropic;  
KW antiangular; cardiant; antibacterial; virucide; fungicide; antileprotic;  
KW protozoacide; cytostatic; neuroprotective; antiparkinsonian; nootropic;  
KW human; diagnosis; therapy; TNV14; monoclonal antibody; mAb.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..19  
FT /label= Signal\_peptide  
FT /note= "amino acids 1-7 are PCR primer-encoded and may  
FT differ from the native sequence"  
FT Protein 20..146  
FT /label= Mature\_protein  
FT Region 31..49  
FT /label= FR1  
FT Region 50..54  
FT /label= CDR1  
FT Region 55..68  
FT /label= FR2  
FT Region 69..85  
FT /label= CDR2  
FT Region 86..117  
FT /label= FR3  
FT Region 118..135  
FT /label= CDR3  
FT Misc-difference 126  
FT /note= "encoded by A"  
FT Region 136..146  
FT /label= J6  
XX  
PN WO200212502-A2.  
XX  
PD 14-FEB-2002.  
XX  
PF 07-AUG-2001; 2001WO-US024785.  
XX  
PR 07-AUG-2000; 2000US-0223360P.  
PR 29-SEP-2000; 2000US-0236826P.  
PR 01-AUG-2001; 2001US-00920137.  
XX  
PA (CENZ ) CENTOCOR INC.  
XX  
PI Giles-Komar J, Knight DM, Heavner G, Scallan B, Shealy D;  
XX WPI; 2002-217194/27.  
DR N-PSDB; ABL53508.  
XX  
PT Novel isolated mammalian anti-tumor necrosis factor antibody, useful for  
PT treating sickle cell anemia, diabetes, atherosclerosis, restenosis,  
PT angina pectoris, myocardial infarction, leprosy.  
XX  
PS Example 3; Fig 4; 131pp; English.  
XX  
CC The present sequence is that of the heavy chain variable region of. anti-  
CC tumour necrosis factor (TNF) human recombinant monoclonal antibody (mAb)  
CC TNV14. TNV14 was 1 of 8 human mAbs produced from a GentNV fusion using  
CC spleen cells from a hybrid mouse containing human variable and constant  
CC region antibody transgenes that was immunised with human TNF alpha. The  
CC human mAbs bound immobilised human TNF alpha with high avidity and had a  
CC totally human IgG1, kappa isotype. They showed relatedness to each other  
CC and to the human germline DP-46 heavy chain sequence (see AAM51167). The

CC invention provides isolated human, primate, rodent, mammalian, chimeric,  
CC humanised and/or complementarity determining region (CDR)-grafted anti-  
CC TNF antibodies, immunoglobulins, cleavage products and other specified  
CC portions and variants, as well as anti-TNF antibody compositions,  
CC encoding or complementary nucleic acids, vectors, host cells,  
CC compositions, formulations, devices, transgenic animals, transgenic  
CC plants, and methods of making and using them. The anti-TNF antibody  
CC comprises at least a portion of an immunoglobulin molecule, especially  
CC the heavy chain and/or light chain variable regions given in the present  
CC sequence and in AAM51165, or either all of the CDRs of the heavy chain  
CC (see AAM51158-60) or all of the CDRs of the light chain (see AAM51161-  
CC 63). The antibodies may inhibit TNF-induced cell adhesion molecules,  
CC inhibit TNF binding to receptor, or provide Arthritic Index improvement  
CC in a mouse model. They are useful for diagnosing or treating a TNF  
CC related condition in a cell, tissue, organ or animal (claimed) such as  
CC rheumatoid arthritis, gastric ulcer, asthma, allergic rhinitis, Crohn's  
CC pathology, sickle cell anaemia, diabetes, a cardiovascular disease such  
CC as arteriosclerosis, atherosclerosis, restenosis, angina pectoris or  
CC myocardial infarction, an infectious disease in a cell such as bacterial,  
CC viral, and fungal infections, pneumonia, leprosy and malaria, a malignant  
CC disease such as leukaemia, chronic myelocytic leukaemia, Burkitt's  
CC lymphoma and multiple myeloma, or a neurological disease such as multiple  
CC sclerosis, Parkinson's disease, spinal ataxia, Alzheimer's disease and  
CC Creutzfeldt-Jakob disease  
XX  
SQ Sequence 146 AA;  
Query Match 92.1%; Score 615.5; DB 5; Length 146;  
Best Local Similarity 92.9%; Pred. No. 3e-45;  
Matches 118; Conservative 3; Mismatches 5; Indels 1; Gaps 1;  
QY 1 QVQLVESGGGVQPGRSRLRLSCAASGFIFSSYAMHWVRQAPGNGLEWVAFMSYDGSNKKY 60  
Db ||||| 20 QVQLVESGGGVQPGRSRLRLSCAASGFTFSSYAMHWVRQAPGKLEWVAIILYDGSKKY 79  
QY 61 ADSVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYVCARDRGIAAGGN-YYYYGM DVWGQ 119  
Db ||||| 80 ADSVKDRFTISRDN SKNTLYLQMN SLRAEDTAVYVCARDRGISAGNYYYGM DVWGQ 139  
QY 120 TTVTVSS 126  
Db ||||| 140 TTVTVSS 146  
RESULT 6  
ADD28320  
ID ADD28320 standard; protein; 135 AA.  
XX  
AC ADD28320;  
XX  
DT 15-JAN-2004 (first entry)  
XX  
DE Human heterodimeric antibody heavy chain variable region SEQ ID NO:98.  
XX  
KW human heterodimeric antibody; human; antibody; binding affinity;  
KW protective antigen; Bacillus anthracis; anthrax infection; cell receptor;  
KW edema factor; lethal factor; virucide; antibacterial; immunotherapy;  
KW anti-toxin; anti-infective; anthrax; botulinum; smallpox;  
KW Venezuelan equine encephalomyelitis virus; VEEV; West Nile virus; WNV.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN WO2003076568-A2.  
XX  
PD 18-SEP-2003.  
XX  
PF 11-FEB-2003; 2003WO-US004206.  
XX  
PR 11-FEB-2002; 2002US-0356086P.  
PR 29-APR-2002; 2002US-0376408P.  
PR 27-SEP-2002; 2002US-0414053P.  
PR 25-NOV-2002; 2002US-0428807P.











QY 61 ADSVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCARDRGIAAGGN-YYYYGMDVWGQG 119  
| | | | | | | | | | | | | | | | | | | | | | : | | | | | | | | | |  
Db 202 ADSVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAKDMGSGWRPYYYYGMDVWGQG 261  
| | | | | | | | | | | | | | | | | | | | | | : | | | | | | | | | |  
QY 120 TTVTVSS 126  
| | | | | | | | | | | | | | | | | | | | | | : | | | | | | | | | |  
Db 262 TTVTVSS 268  
| | | | | | | | | | | | | | | | | | | | | | : | | | | | | | | | |  
RESULT 14  
AAAY44995  
ID AAY44995 standard; protein; 524 AA.  
XX  
AC AAY44995;  
XX  
DT 23-MAY-2000 (first entry)  
XX  
DE HD70scFv-Ck-interleukin 2.  
XX  
KW HD70; single-chain Fv fragment; scFv; antibody; 17-1A antigen; human;  
KW EPCAM; epithelial cell adhesion molecule; inflammatory cytokine; IL-2;  
KW interleukin-2; Ck-domain; kappa light chain constant domain;  
KW heteromiribody; multifunctional compound; immunoglobulin; cytostatic;  
KW immunostimulatory; antileukaemia; diagnosis; prevention;  
KW antiproliferative; treatment; malignant; haematopoietic cell; lymphoma;  
KW leukaemia; solid tumour; carcinoma; melanoma; sarcoma.  
XX  
OS Homo sapiens.  
XX  
PN WO200006605-A2.  
XX  
PD 10-FEB-2000.  
XX  
PF 28-JUL-1999; 99WO-EP005416.  
XX  
PR 28-JUL-1998; 98EP-00114082.  
XX  
PA (MICR-) MICROMET GES BIOMEDIZINISCHE FORSCHUNG.  
XX  
PI Kufer P, Dreier T, Baeuerle PA, Borschert K, Zettl F;  
XX WPI; 2000-195265/17.  
DR N-PSDB; AAZ50588.  
XX  
PT New multifunctional compounds useful for preventing and/or treating  
PT malignant cell growth and for detection and diagnosis.  
XX  
PS Example 10; Fig 55B; 166pp; English.  
XX  
CC The patent discloses heteromiribodies which are multifunctional compounds  
CC producible in a mammalian host cell as a secretable and fully functional  
CC heterodimer of two polypeptide chains, where one of the polypeptide  
CC chains comprises, a CH1-domain (constant domain of an immunoglobulin  
CC heavy chain) and the other chain comprises CL-domain (constant domain of  
CC an immunoglobulin light chain). The polypeptide chains further comprise,  
CC fused to the constant domains at least two (poly)peptides having  
CC different receptor or ligand functions, where further at least two of the  
CC different (poly)peptides lack an intrinsic affinity for one another and  
CC are linked via the constant domains. The heteromiribodies have  
CC cytostatic, immunostimulatory, antileukaemia and antiproliferative  
CC activities. These compounds can be used for diagnosing, preventing and  
CC treating malignant cell growth related to malignancies of haematopoietic  
CC cells e.g. lymphomas and leukaemias, or to solid tumours e.g. carcinomas,  
CC melanomas and sarcomas. The present sequence is the right chain of a  
CC heteromiribody comprising HD70 single-chain Fv (scFv) fragment N-  
CC terminally linked to human Ck domain (constant domain of immunoglobulin-  
CC kappa light chain) which bears at its C-terminus the human inflammatory  
CC cytokine interleukin-2 (IL-2). HD70 scFv specifically recognises the  
CC human epithelial cell adhesion molecule (EPCAM) also called 17-1A antigen  
XX  
SQ Sequence 524 AA;

Query Match 87.1%; Score 581.5; DB 3; Length 524;

Best Local Similarity 87.4%; Pred. No. 9.3e-42;  
Matches 111; Conservative 5; Mismatches 10; Indels 1; Gaps 1;  
QY 1 QVQLVESGGGVQPGKSLRLSCAASGFISSYAMHWVRQAPGNGLEWVAFMSYDGSNKKY 60  
: | | | | | | | | | | | | | | | | | | | | | | : | | | | | | | | | |  
Db 142 EVQLLES GGVQPGKSLRLSCAASGFTSSYGMHWVRQAPGKGLEWAVISYDGSNKYY 201  
: | | | | | | | | | | | | | | | | | | | | | | : | | | | | | | | | |  
QY 61 ADSVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCARDRGIAAGGN-YYYYGMDVWGQG 119  
| | | | | | | | | | | | | | | | | | | | | | : | | | | | | | | | |  
Db 202 ADSVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAKDMGSGWRPYYYYGMDVWGQG 261  
| | | | | | | | | | | | | | | | | | | | | | : | | | | | | | | | |  
QY 120 TTVTVSS 126  
| | | | | | | | | | | | | | | | | | | | | | : | | | | | | | | | |  
Db 262 TTVTVSS 268  
| | | | | | | | | | | | | | | | | | | | | | : | | | | | | | | | |  
RESULT 15  
ADK18593  
ID ADK18593 standard; protein; 126 AA.  
XX  
AC ADK18593;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE Anti-human PDGF-D antibody heavy chain protein sequence.  
XX  
KW antiinflammatory; immunomodulator; cytostatic; gene therapy.  
XX  
OS Homo sapiens.  
XX  
PN WO2003057857-A2.  
XX  
PD 17-JUL-2003.  
XX  
PF 06-JAN-2003; 2003WO-US000398.  
XX  
PR 07-JAN-2002; 2002US-00041860.  
XX  
PA (ABGE-) ABGENIX INC.  
XX  
PI Corvalan JRP, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;  
PI Bezabeh B;  
XX  
DR WPI; 2003-587119/55.  
XX  
PT New human monoclonal antibody that binds to platelet-derived growth  
PT factor-D (PDGF-D), useful for treating chronic and recurrent human  
PT diseases, such as inflammation, autoimmunity and cancer.  
XX  
PS Disclosure; SEQ ID NO 17; 255pp; English.  
XX  
CC The invention relates to a human monoclonal antibody that binds to  
CC platelet-derived growth factor-D (PDGF-D). The antibodies are useful for  
CC treating chronic and recurrent human diseases, such as inflammation,  
CC autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are  
CC useful for modulating collagen formation, and for staging various  
CC cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were  
CC generated using an active protein fragment of the gene product from the  
CC clone 30664188.0.99 arising in the conditioned medium obtained when  
CC HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This  
CC sequence corresponds to a protein used in the invention.  
XX  
SQ Sequence 126 AA;

Query Match 87.0%; Score 581; DB 7; Length 126;  
Best Local Similarity 88.1%; Pred. No. 2.4e-42;  
Matches 111; Conservative 3; Mismatches 12; Indels 0; Gaps 0;

QY 1 QVQLVESGGGVQPGKSLRLSCAASGFISSYAMHWVRQAPGNGLEWVAFMSYDGSNKKY 60  
| | | | | | | | | | | | | | | | | | | | | | : | | | | | | | | | |  
Db 1 QVQLVESGGGVQPGKSLRLSCAASGFTSSYGMHWVRQAPGKGLEWAVIYDGSNKYY 60  
| | | | | | | | | | | | | | | | | | | | | | : | | | | | | | | | |  
QY 61 ADSVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCARDRGIAAGGNYYYYGMDVWGQG 120

Db	61	ADSVKGRFTISRDN SKNTLYLQMSLR AEDTAVYYCARDQGYRYAGYYDYGM DVGQGT	120
Qy	121	TVTVSS	126
Db	121	TVTVSS	126

Search completed: December 28, 2005, 13:58:06  
Job time : 149.538 secs

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OM protein - protein search, using sw model

Run on: December 28, 2005, 13:46:34 ; Search time 25.8462 Seconds  
(without alignments)  
469.057 Million cell updates/sec

Title: US-09-920-137F-7  
Perfect score: 668  
Sequence: 1 QVQLVESGGGVQPGKSLRL.....NYYVGMDEVWGQGTTVTSS 126

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	577	86.4	122	2 E36005	Ig heavy chain V r
2	575	86.1	128	2 S48797	Ig heavy chain V r
3	563.5	84.4	123	2 S38493	Ig heavy chain - h
4	539.5	80.8	119	2 F36005	Ig heavy chain V r
5	537	80.4	118	2 S31116	Ig heavy chain - h
6	534.5	80.0	121	2 G36005	Ig heavy chain V r
7	533	79.8	147	2 I37780	Ig variable region
8	532.5	79.7	133	2 A49028	Ig heavy chain V-I
9	532	79.6	114	2 S46390	Ig heavy chain V r
10	530.5	79.4	132	2 S31603	Ig heavy chain V r
11	529.5	79.3	121	2 S19666	Ig heavy chain V r
12	528.5	79.1	134	2 S31679	Ig heavy chain V r
13	528	79.0	140	2 S70442	Ig heavy chain pre
14	524	78.4	114	2 S46392	Ig heavy chain V r
15	524	78.4	122	2 S31117	Ig heavy chain - h
16	519	77.7	120	2 S31112	Ig heavy chain pre
17	515.5	77.2	160	2 S05271	Ig heavy chain V r
18	515	77.1	118	2 PH1660	Ig heavy chain V r
19	514	76.9	137	2 S31701	Ig heavy chain V r
20	514	76.9	139	2 S31674	Ig heavy chain V r
21	512.5	76.7	130	2 PL0098	Ig heavy chain pre
22	511.5	76.6	125	2 S37455	Ig mu chain - huma
23	510.5	76.4	130	2 S31601	Ig heavy chain V r
24	509.5	76.3	135	2 S31598	Ig heavy chain V r
25	507.5	76.0	117	2 S36259	Ig heavy chain V r
26	507	75.9	122	1 M3HUAM	Ig heavy chain V-I
27	504.5	75.5	111	2 PH1645	Ig heavy chain V r
28	503	75.3	114	2 S46391	Ig heavy chain V r
29	499.5	74.8	117	2 S36270	Ig heavy chain V r

30	499	74.7	133	2 S31510	Ig heavy chain - h
31	495.5	74.2	109	2 PH1646	Ig heavy chain V r
32	494.5	74.0	109	2 PH1644	Ig heavy chain V r
33	494.5	74.0	123	2 S26794	Ig heavy chain V r
34	493	73.8	118	2 PH1662	Ig heavy chain V r
35	493	73.8	126	1 G1HUKL	Ig heavy chain V-I
36	492	73.7	145	2 S11239	Ig heavy chain V r
37	491.5	73.6	113	2 S38490	Ig heavy chain - h
38	490	73.4	151	2 A60943	Ig heavy chain pre
39	489.5	73.3	122	2 S31119	Ig heavy chain - h
40	489	73.2	108	2 PH1642	Ig heavy chain V r
41	487.5	73.0	119	2 S31107	Ig heavy chain - h
42	487.5	73.0	121	2 PH1661	Ig heavy chain V r
43	487.5	73.0	125	2 S30531	Ig heavy chain V r
44	486.5	72.8	111	2 PH1643	Ig heavy chain V r
45	485.5	72.7	127	2 S38489	Ig heavy chain - h

ALIGNMENTS

RESULT 1  
E36005  
Ig heavy chain V region (M72) - human  
C;Species: Homo sapiens (man)  
C;Date: 21-Dec-1990 #sequence\_revision 21-Dec-1990 #text\_change 16-Dec-1998  
C;Accession: E36005  
R;Schroeder Jr., H.W.; Wang, J.Y.  
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990  
A;Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene  
A;Reference number: A36005; MUID:90349571; PMID:2117273  
A;Accession: E36005  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-122 <SCH>  
A;Cross-references: UNIPARC:UPI0000176C30; GB:M34030  
C;Genetics:  
A;Gene: GDB:IGH@; IGHDY1  
A;Cross-references: GDB:118731; OMIM:146910  
A;Map position: 14q32.33-14q32.33  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match	86.4%;	Score 577;	DB 2;	Length 122;
Best Local Similarity	88.9%;	Pred. No. 6.9e-45;		
Matches 112;	Conservative	4;	Mismatches 6;	Indels 4; Gaps 1;
QY	1	QVQLVESGGGVQPGKSLRLSCAASGIFSSYAMHWVRQAPGNGLEWVAFMSYDGSNKKY	60	
Db	1	QVQLVESGGGVQPGKSLRLSCAASGFTFSYAMHWVRQAPGKLEWVAISYDGSNKKY	60	
QY	61	ADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDRGIAAGNYYYGMDVWGQGT	120	
Db	61	ADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDRHSSS----WYYGMDVWGQGT	116	
QY	121	TVTSS 126		
Db	117	TVTSS 122		

RESULT 2  
S48797  
Ig heavy chain V region (anti-Sm, VH3/Dxp4/JH6) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 13-Jan-1995 #sequence\_revision 13-Sep-1998 #text\_change 23-Jul-1999  
C;Accession: S48797; S26893  
R;Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.  
submitted to the EMBL Data Library, October 1994  
A;Description: Molecular characterization of natural human anti-Sm autoantibodies.  
A;Reference number: S48797  
A;Accession: S48797  
A;Molecule type: mRNA





RESULT 10  
S31603  
Ig heavy chain V region - human  
C;Species: Homo sapiens (man)  
C;Date: 03-Mar-1994 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C;Accession: S31603  
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelles, C.  
submitted to the EMBL Data Library, June 1992  
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the  
A;Reference number: S31585  
A;Accession: S31603  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-132 <CUI>  
A;Cross-references: UNIPARC:UPI0000116455; EMBL:Z14168; NID:g30999; PIDN:CAA78537.1; PID  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;30-113/Domain: immunoglobulin homology <IMM>  
  
Query Match 79.4%; Score 530.5; DB 2; Length 132;  
Best Local Similarity 82.5%; Pred. No. 1.1e-40;  
Matches 104; Conservative 4; Mismatches 9; Indels 9; Gaps 2;  
  
QY 1 QVQLVESGGGVQPGRSRLRLSCAASGFIFSSYAMHWVRQAPGNGLEWVAFMSYDGSNKYY 60  
Db 16 QVQLVESGGGVQPGRSRLRLSCAASGFTFSSYGMHWVRQAPGKLEWVAVISYDGSNKYY 75  
  
QY 61 ADSVKGRFTISRDNKNTLYQMNSLRAEDTAVYYCARDRGIAAGGNYYYGMDVWGQGT 120  
Db 76 ADSVKGRFTISRDNKNTLYQMNSLRAEDTAVYYCAKDL-----FYFF--DYWGQGT 126  
  
QY 121 TTVTSS 126  
Db 127 LVTVSS 132  
  
RESULT 11  
S19666  
Ig heavy chain V region (VH3DJH4) - human  
C;Species: Homo sapiens (man)  
C;Date: 22-Jan-1993 #sequence\_revision 22-Jan-1993 #text\_change 20-Jun-2000  
C;Accession: S19666  
R;Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter,  
J. Mol. Biol. 222, 581-597, 1991  
A;Title: By-passing immunization. Human antibodies from V-gene libraries displayed on ph  
A;Reference number: S19663; MUID:92085276; PMID:1748994  
A;Accession: S19666  
A;Molecule type: mRNA  
A;Residues: 1-121 <MAR>  
A;Cross-references: UNIPARC:UPI0000115FE5; EMBL:X61646; NID:g37688; PIDN:CAA43827.1; PID  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>  
  
Query Match 79.3%; Score 529.5; DB 2; Length 121;  
Best Local Similarity 82.5%; Pred. No. 1.2e-40;  
Matches 104; Conservative 6; Mismatches 11; Indels 5; Gaps 2;  
  
QY 1 QVQLVESGGGVQPGRSRLRLSCAASGFIFSSYAMHWVRQAPGNGLEWVAFMSYDGSNKYY 60  
Db 1 QVQLVQSGGGVQPGRSRLRLSCAASGFTFSSYGMHWVRQAPGKLEWVAVISYDGSNKYY 60  
  
QY 61 ADSVKGRFTISRDNKNTLYQMNSLRAEDTAVYYCARDRGIAAGGNYYYGMDVWGQGT 120  
Db 61 ADSVKGRFTISRDNKNTLYQMNSLRAEDTAVYYCAK-TGYSSGWGYF----DYWGQGT 115  
  
QY 121 TTVTSS 126  
Db 116 LVTVSS 121  
  
RESULT 12

S31679  
Ig heavy chain V region - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C;Accession: S31679  
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelles, C.  
submitted to the EMBL Data Library, June 1992  
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the  
A;Reference number: S31585  
A;Accession: S31679  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-134 <CUI>  
A;Cross-references: UNIPARC:UPI0000116475; EMBL:Z14203; NID:g30965; PIDN:CAA78572.1; PID  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;34-117/Domain: immunoglobulin homology <IMM>  
  
Query Match 79.1%; Score 528.5; DB 2; Length 134;  
Best Local Similarity 83.5%; Pred. No. 1.7e-40;  
Matches 106; Conservative 2; Mismatches 6; Indels 13; Gaps 2;  
  
QY 1 QVQLVESGGGVQPGRSRLRLSCAASGFIFSSYAMHWVRQAPGNGLEWVAFMSYDGSNKYY 60  
Db 20 QVQLVESGGGVQPGRSRLRLSCAASGFTFSSYAMHWVRQAPGKLEWVAVISYDGSNKYY 79  
  
QY 61 ADSVKGRFTISRDNKNTLYQMNSLRAEDTAVYYCARD-RGIAAGGNYYYGMDVWGQG 119  
Db 80 ADSVKGRFTISRDNKNTLYQMNSLRAEDTAVYYCARESG-----DYWGQG 127  
  
QY 120 TTVTSS 126  
Db 128 TLVTSS 134  
  
RESULT 13  
S70442  
Ig heavy chain precursor V region (mu) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 24-Jul-1998 #sequence\_revision 24-Jul-1998 #text\_change 31-Dec-2004  
C;Accession: S70442  
R;Cuisinier, A.M.; Fumoux, F.; Fougereau, M.; Tonnelles, C.  
Mol. Immunol. 29, 1363-1373, 1992  
A;Title: IgM kappa/lambda EBV human B cell clone: an early step of differentiation of fe  
A;Reference number: S70442; MUID:93024508; PMID:1383695  
A;Accession: S70442  
A;Status: not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-140 <CUI>  
A;Cross-references: UNIPROT:Q8WUK1; UNIPARC:UPI0000176EB7  
C;Superfamily: immunoglobulin homology  
F;34-117/Domain: immunoglobulin homology <IMM>  
  
Query Match 79.0%; Score 528; DB 2; Length 140;  
Best Local Similarity 82.5%; Pred. No. 2e-40;  
Matches 104; Conservative 3; Mismatches 13; Indels 6; Gaps 2;  
  
QY 1 QVQLVESGGGVQPGRSRLRLSCAASGFIFSSYAMHWVRQAPGNGLEWVAFMSYDGSNKYY 60  
Db 20 QVQLVESGGGVQPGSRLRLSCAASGFTFSSYGMHWVRQAPGKLEWVAFIRDGSNKYY 79  
  
QY 61 ADSVKGRFTISRDNKNTLYQMNSLRAEDTAVYYCARDRGIAAGGNYYYGMDVWGQGT 120  
Db 80 ADSVKGRFTISRDNKNTLYQMNSLRAEDTAVYYCARDH--IVGATYF-----DYWGQGT 133  
  
QY 121 TTVTSS 126  
Db 134 LVTSS 139  
  
RESULT 14  
S46392  
Ig heavy chain V region (VH-28) - human



C;Species: Homo sapiens (man)  
C;Date: 27-Jan-1995 #sequence\_revision 27-Jan-1995 #text\_change 20-Jun-2000  
C;Accession: S46392  
R;Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.  
J. Mol. Biol. 239, 68-78, 1994  
A;Title: In vitro assembly of repertoires of antibody chains on the surface of phage by  
A;Reference number: S46390; MUID:94254092; PMID:8196048  
A;Accession: S46392  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-114 <FIG>  
A;Cross-references: UNIPARC:UPI00001137D6; EMBL:Z31688; NID:g499306; PIDN:CAA83493.1; PI  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match	78.4%	Score 524;	DB 2;	Length 114;
Best Local Similarity	82.5%	Pred. No. 3.6e-40;		
Matches 104;	Conservative 1;	Mismatches 9;	Indels 12;	Gaps 1;

  

Qy	1	QVQLVESGGGVQPGKSLRLS	CAASGFIFSSYAMHWVRQAPGNGLEWVAFMSYDGSNKKY	60
Db	1	QVNLRESGGGVQPGKSLRLS	CAASGFTFSSYAMHWVRQAPGKLEWVAVISYDGSNKYY	60

  

Qy	61	ADSVKGRFTISRDN	SKNTLYLQMN	SLRAEDTAVYYCARD	RGIAAGNYYYGMDVWGQGT	120
Db	61	ADSVKGRFTISRDN	SKNTLYLQMN	SLRAEDTAVYYCARD	SG-----GYWGQGT	108

  

Qy	121	TVT	VSS	126
Db	109	TVT	VSS	114

RESULT 15  
S31117  
Ig heavy chain - human  
C;Species: Homo sapiens (man)  
C;Date: 02-Dec-1993 #sequence\_revision 26-May-1995 #text\_change 17-Mar-1999  
C;Accession: S31117  
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman  
Eur. J. Immunol. 22, 247-251, 1992  
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple  
A;Reference number: S31104; MUID:92111633; PMID:1730252  
A;Accession: S31117  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-122 <RAA>  
A;Cross-references: UNIPARC:UPI0000176C8D; EMBL:X62967  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match	78.4%	Score 524;	DB 2;	Length 122;
Best Local Similarity	83.3%	Pred. No. 3.9e-40;		
Matches 105;	Conservative 4;	Mismatches 13;	Indels 4;	Gaps 2;

  

Qy	1	QVQLVESGGGVQPGKSLRLS	CAASGFIFSSYAMHWVRQAPGNGLEWVAFMSYDGSNKKY	60
Db	1	QVQLVESGGGVQPGKSLRLS	CAASGFTFSSYGMHWVRQAPGKLEWVAWIYDGSNKYY	60

  

Qy	61	ADSVKGRFTISRDN	SKNTLYLQMN	SLRAEDTAVYYCARD	RGIAAGNYYYGMDVWGQGT	120
Db	61	ADSVKGRFTISRDN	SKNTLYLQMN	SLRAEDTAVYYCARD	--FFAPPNWSHF--DYWGQGT	116

  

Qy	121	TVT	VSS	126
Db	117	LVT	VSS	122

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## Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.

- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

**When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.**

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 28, 2005, 13:44:24 ; Search time 159.923 Seconds  
(without alignments)  
555.871 Million cell updates/sec

Title: US-09-920-137F-7  
Perfect score: 668  
Sequence: 1 QVQLVESGGGVVQPGKSLRL.....NYYYYGMDVWGQGITVTVSS 126

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_05.80:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	528	79.0	613	2 Q8WUK1_HUMAN	Q8wuk1 homo sapien
2	520.5	77.9	472	2 Q6N089_HUMAN	Q6n089 homo sapien
3	518.5	77.6	116	2 Q9UL93_HUMAN	Q9ul93 homo sapien
4	518	77.5	606	2 Q6GMV2_HUMAN	Q6gmv2 homo sapien
5	514.5	77.0	240	2 Q65ZC9_HUMAN	Q65zcg homo sapien
6	513.5	76.9	113	2 Q9UL90_HUMAN	Q9ul90 homo sapien
7	510	76.3	573	2 Q8WU38_HUMAN	Q8wu38 homo sapien
8	507	75.9	122	1 HV3G_HUMAN	P01768 homo sapien
9	503	75.3	147	2 Q9Y509_HUMAN	Q9y509 homo sapien
10	501.5	75.1	478	2 Q6PI81_HUMAN	Q6pi81 homo sapien
11	493	73.8	126	1 HV3K_HUMAN	P01772 homo sapien
12	485	72.6	122	2 Q9UL84_HUMAN	Q9ul84 homo sapien
13	484.5	72.5	597	2 Q96BB9_HUMAN	Q96bb9 homo sapien
14	480	71.9	544	2 Q6PJ95_HUMAN	Q6pj95 homo sapien
15	479	71.7	122	1 HV3H_HUMAN	P01769 homo sapien
16	479	71.7	469	2 Q569F4_HUMAN	Q569f4 homo sapien
17	477.5	71.5	119	1 HV3I_HUMAN	P01770 homo sapien
18	475.5	71.2	464	2 Q6MZU6_HUMAN	Q6mzu6 homo sapien
19	475.5	71.2	470	2 Q6PJA4_HUMAN	Q6pja4 homo sapien
20	470.5	70.4	121	2 Q9UL71_HUMAN	Q9ul71 homo sapien
21	470	70.4	136	1 HV16_MOUSE	P01783 mus musculu
22	469.5	70.3	121	1 HV3J_HUMAN	P01771 homo sapien
23	465	69.6	475	2 Q5EFE5_HUMAN	Q5efe5 homo sapien
24	463.5	69.4	493	2 Q6GMX2_HUMAN	Q6gmxx2 homo sapien
25	463.5	69.4	519	2 Q6N092_HUMAN	Q6n092 homo sapien
26	459.5	68.8	493	2 Q8NCL6_HUMAN	Q8ncl6 homo sapien
27	459.5	68.8	499	2 Q8N5K4_HUMAN	Q8n5k4 homo sapien
28	457	68.4	467	2 Q4VBH1_RAT	Q4vbh1 rattus norv
29	452	67.7	465	2 Q5I0J0_RAT	Q5i0j0 rattus norv
30	451	67.5	118	2 Q9UL91_HUMAN	Q9ul91 homo sapien
31	450.5	67.4	482	2 Q7Z351_HUMAN	Q7z351 homo sapien

32	450	67.4	479	2 Q6MZV6_HUMAN	Q6mzv6 homo sapien
33	446	66.8	475	2 Q6GMW7_HUMAN	Q6gmw7 homo sapien
34	445	66.6	112	2 Q9HCC1_HUMAN	Q9hcc1 homo sapien
35	443	66.3	116	1 HV3T_HUMAN	P01781 homo sapien
36	443	66.3	461	2 Q5M7V3_RAT	Q5m7v3 rattus norv
37	441.5	66.1	470	2 Q68CN4_HUMAN	Q68cn4 homo sapien
38	441	66.0	118	2 Q9UL72_HUMAN	Q9ul72 homo sapien
39	439.5	65.8	479	2 Q5BK12_RAT	Q5bk12 rattus norv
40	437	65.4	473	2 Q6MZV7_HUMAN	Q6mzv7 homo sapien
41	436	65.3	465	2 Q6P6C4_HUMAN	Q6p6c4 homo sapien
42	436	65.3	475	2 Q6MZQ6_HUMAN	Q6mzq6 homo sapien
43	436	65.3	487	2 Q99KA4_MOUSE	Q99ka4 mus musculu
44	436	65.3	494	2 Q96K68_HUMAN	Q96k68 homo sapien
45	435.5	65.2	485	2 Q6PDB8_MOUSE	Q6pdb8 mus musculu

ALIGNMENTS

RESULT 1  
Q8WUK1\_HUMAN  
ID Q8WUK1\_HUMAN PRELIMINARY; PRT; 613 AA.  
AC Q8WUK1;  
DT 01-MAR-2002 (TremBLrel. 20, Created)  
DT 01-MAR-2002 (TremBLrel. 20, Last sequence update)  
DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)  
DE IGHM protein.  
GN Name=IGHM;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Primary B-Cells;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smalusz D.E.,  
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Primary B-Cells;  
RG NIH MGC Project;  
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=2117273;  
RA Schroeder H.W. Jr, Wang J.Y.;  
RT "Preferential utilization of conserved immunoglobulin heavy chain  
variable gene segments during human fetal life.";  
RL Proc. Natl. Acad. Sci. U.S.A. 87:6146-6150(1990).  
RN [4]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=1383695; DOI=10.1016/0161-5890(92)90173-U;  
RA Cuisinier A.M., Fumoux F., Fougereau M., Tonnelle C.;

RT "IGM kappa/lambda EBV human B cell clone: an early step of  
RT differentiation of fetal B cells or a distinct B lineage?";  
RL Mol. Immunol. 29:1363-1373(1992).  
RN [5]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=1730252;  
RA Raaphorst F.M., Timmers E., Kenter M.J., Van Tol M.J., Vossen J.M.,  
RA Schuurman R.K.;  
RT "Restricted utilization of germ-line VH3 genes and short diverse third  
RT complementarity-determining regions (CDR3) in human fetal B lymphocyte  
RT immunoglobulin heavy chain rearrangements.";  
RL Eur. J. Immunol. 22:247-251(1992).  
RN [6]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=1904154;  
RA Neale G.A., Kitchingman G.R.;  
RT "mRNA transcripts initiating within the human immunoglobulin mu heavy  
RT chain enhancer region contain a non-translatable exon and are  
RT extremely heterogeneous at the 5' end.";  
RL Nucleic Acids Res. 19:2427-2433(1991).  
RN [7]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=2840480; DOI=10.1084/jem.168.1.229;  
RA Dird J., Galili N., Link M., Stites D., Sklar J.;  
RT "Continuing rearrangement but absence of somatic hypermutation in  
RT immunoglobulin genes of human B cell precursor leukemia.";  
RL J. Exp. Med. 168:229-245(1988).  
RN [8]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=2538551; DOI=10.1084/jem.169.4.1391;  
RA Nickerson K.G., Berman J., Glickman E., Chess L., Alt F.W.;  
RT "Early human Igh gene assembly in Epstein-Barr virus-transformed fetal  
RT B cell lines. Preferential utilization of the most JH-proximal D  
RT segment (DQ52) and two unusual VH-related rearrangements.";  
RL J. Exp. Med. 169:1391-1403(1989).  
RN [9]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=93301610; PubMed=8315388; DOI=10.1084/jem.178.1.331;  
RA Hillson J.L., Karr N.S., Opplinger I.R., Mannik M., Sasso E.H.;  
RT "The structural basis of germline-encoded VH3 immunoglobulin binding  
RT to staphylococcal protein A.";  
RL J. Exp. Med. 178:331-336(1993).  
DR EMBL; BC020240; AAH20240.1; -; mRNA.  
DR PIR; F36005; F36005.  
DR PIR; G36005; G36005.  
DR PIR; PH1642; PH1642.  
DR PIR; PH1643; PH1643.  
DR PIR; PH1645; PH1645.  
DR PIR; PH1646; PH1646.  
DR PIR; PL0098; PL0098.  
DR PIR; PL0120; PL0120.  
DR PIR; S15590; S15590.  
DR PIR; S31116; S31116.  
DR PIR; S31119; S31119.  
DR PIR; S70442; S70442.  
DR HSSP; P01861; 1ADQ.  
DR SMR; Q8WUK1; 20-242.  
DR Ensembl; ENSG00000130076; Homo sapiens.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig\_cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF07654; C1-set; 4.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 5.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_3.  
KW Immunoglobulin domain.  
SQ SEQUENCE 613 AA; 67296 MW; 60C7F5950671E315 CRC64;

Query Match 79.0%; Score 528; DB 2; Length 613;  
Best Local Similarity 81.2%; Pred. No. 2.2e-44;  
Matches 104; Conservative 4; Mismatches 10; Indels 10; Gaps 2;

QY 1 QVQLVESGGGVVQPGRSRLRLSCAASGFISSYAMHWVRQAPGNGLWVAFMSYDGSNKKY 60  
Db |||||  
20 QVQLVESGGGVVQPGRSRLRLSCAASGFTFSSYGMHWVRQAPGKLEWAVISYDGSNKYY 79  
QY 61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARD--RGIAAGNYYYGMVDVWGQ 118  
Db |||||  
80 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKDWSEGVET-----FDIWGQ 131  
QY 119 GTTVTVSS 126  
Db |||||  
132 GTMTVTSS 139  
RESULT 2  
Q6N089\_HUMAN  
ID Q6N089\_HUMAN PRELIMINARY; PRT; 472 AA.  
AC Q6N089;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein DKFzp686P15220.  
GN Name=DKFzp686P15220;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Rectum tumor;  
RG The German cDNA Consortium;  
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,  
RA Fobo G., Han M., Wiemann S.;  
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BX640627; CAE45781.1; -; mRNA.  
DR HSSP; P01861; 1ADQ.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig\_cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF07654; C1-set; 3.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGcl; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
SQ SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;

Query Match 77.9%; Score 520.5; DB 2; Length 472;  
Best Local Similarity 77.8%; Pred. No. 9.4e-44;  
Matches 98; Conservative 12; Mismatches 13; Indels 3; Gaps 1;

QY 1 QVQLVESGGGVVQPGRSRLRLSCAASGFISSYAMHWVRQAPGNGLWVAFMSYDGSNKKY 60  
Db :|||  
20 EVQLVESGGGLVQPGRSRLRLSCAASGFTFDDYAMHWVRQAPGKLEWVSGISGSIAY 79  
QY 61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDRGIAAGNYYYGMVDVWGQGT 120  
Db |||||  
80 ADSVKGRFTISRDNKNSLYLQMNSLRAEDTALYYCAKEIG--AHNFYYIGMDVWGQGT 136  
QY 121 TTVTVSS 126  
Db |||||  
137 TTVTVSS 142

RESULT 3  
Q9UL93\_HUMAN  
ID Q9UL93\_HUMAN PRELIMINARY; PRT; 116 AA.  
AC Q9UL93;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)  
DE Myosin-reactive immunoglobulin heavy chain variable region  
DE (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
RT fetus.";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=93301610; PubMed=8315388; DOI=10.1084/jem.178.1.331;  
RA Hillson J.B., Karr N.S., Opplinger I.R., Mannik M., Sasso E.H.;  
RT "The structural basis of germline-encoded VH3 immunoglobulin binding  
RT to staphylococcal protein A.";  
RL J. Exp. Med. 178:331-336(1993).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=2840480;  
RA Bird J., Galili N., Link M., Stites D., Sklar J.;  
RT "Continuing rearrangement but absence of somatic hypermutation in  
RT immunoglobulin genes of human B cell precursor leukemia.";  
RL J. Exp. Med. 168:229-245(1988).  
DR EMBL; AF035021; AAD56257.1; -; mRNA.  
DR PIR; PH1644; PH1644.  
DR PIR; PLO120; PLO120.  
DR HSSP; P01772; 2FB4.  
DR SMR; Q9UL93; 1-116.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
FT NON\_TER 1  
FT NON\_TER 116 116  
SQ SEQUENCE 116 AA; 12434 MW; 0DA0348154DD6061 CRC64;  
  
Query Match 77.6%; Score 518.5; DB 2; Length 116;  
Best Local Similarity 81.6%; Pred. No. 2.9e-44;  
Matches 102; Conservative 4; Mismatches 10; Indels 9; Gaps 1;  
  
QY 2 VQLVESGGGVQPGRSRLRLSCAASGFIFSSYAMHWVRQAPGNGLEWVAFMSYDGSNKYYA 61  
Db 1 VQLVESGGGVQPGRSRLRLSCAASGFTFSSYAMHWVRQAPGKLEWVAVISYDGSNKYYA 60  
QY 62 DSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDRGIAAGNYYYYGMDVWGQGT 121  
Db 61 DSVKGRFTISRDNKNTLYLQMNSLRAEDTAMYYCAGGGGL-----GLGYWGQGT 111  
QY 122 VTVSS 126  
Db 112 VTVSS 116  
  
RESULT 4  
Q6GMY2 HUMAN  
ID Q6GMY2 HUMAN PRELIMINARY; PRT; 606 AA.  
AC Q6GMY2;  
DT 05-JUL-2004 (TReMBLrel. 27, Created)  
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)  
DE IGHM protein.  
GN Name=IGHM;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.

OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Primary B-Cells;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Primary B-Cells;  
RG NIH MGC Project;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC073758; AAH73758.1; -; mRNA.  
DR SMR; Q6GMY2; 20-256.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig\_c1.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF07654; C1-set; 4.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGc1; 4.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 5.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN 3.  
SQ SEQUENCE 606 AA; 66185 MW; B6B38B51114E4C55 CRC64;  
  
Query Match 77.5%; Score 518; DB 2; Length 606;  
Best Local Similarity 76.1%; Pred. No. 2.2e-43;  
Matches 102; Conservative 8; Mismatches 16; Indels 8; Gaps 2;  
  
QY 1 QVQLVESGGGVQPGRSRLRLSCAASGFIFSSYAMHWVRQAPGNGLEWVAFMSYDGSNKKY 60  
Db 20 QVQLVESGGGLVKPGSRLRLSCAASGFTFSDYMSWIRQAPGKLEWVSYSSTSYNY 79  
QY 61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAR-DRGIAAGN-----YYYYG 112  
Db 80 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARGNGIAAAGRNVVYAEDYYYYYG 139  
QY 113 MDVWGQGTTVTVSS 126  
Db 140 MDVWGQGTTVTVSS 153  
  
RESULT 5  
Q65ZC9 HUMAN  
ID Q65ZC9 HUMAN PRELIMINARY; PRT; 240 AA.  
AC Q65ZC9;  
DT 25-OCT-2004 (TReMBLrel. 28, Created)  
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)  
DE Single-chain Fv (Fragment).  
GN Name=scFv;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C1q/7;  
RX MEDLINE=97362799; PubMed=9219263; DOI=10.1038/nbt0797-629;  
RA Kontermann R.E., Wing M.G., Winter G.;  
RT "Complement recruitment using bispecific diabodies.";  
RL Nat. Biotechnol. 15:629-631(1997).  
DR EMBL; Y13056; CAA73499.1; -; mRNA.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00406; IGV; 2.  
DR PROSITE; PS50835; IG\_LIKE; 2.  
FT NON\_TER 1 240 240  
FT NON\_TER 240 240  
SQ SEQUENCE 240 AA; 25569 MW; FDCFD3645F64B373 CRC64;  
..  
Query Match 77.0%; Score 514.5; DB 2; Length 240;  
Best Local Similarity 80.2%; Pred. No. 1.7e-43;  
Matches 101; Conservative 6; Mismatches 10; Indels 9; Gaps 1;  
  
QY 1 QVQLVESGGGVQPGKSLRLSCAASGFISSYAMHWVRQAPGNGLEWVAFMSYDGSNKKY 60  
Db 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKKY 60  
  
QY 61 ADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDRGIAAGNYYYYGMDVWGQGT 120  
Db 61 ADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDWGDSDS-----LDPWGKGT 111  
  
QY 121 TVTVSS 126  
Db 112 LVTVSS 117  
  
RESULT 6  
Q9UL90 HUMAN  
ID Q9UL90\_HUMAN PRELIMINARY; PRT; 113 AA.  
AC Q9UL90;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).  
DE OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;  
RA "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus.";  
RT Clin. Immunol. Immunopathol. 87:184-192(1998).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=1730252;  
RA Raaphorst F.M., Timmers E., Kenter M.J., Van Tol M.J., Vossen J.M., Schuurman R.K.;  
RA "Restricted utilization of germ-line VH3 genes and short diverse third complementarity-determining regions (CDR3) in human fetal B lymphocyte immunoglobulin heavy chain rearrangements.";  
RL Eur. J. Immunol. 22:247-251(1992).  
DR EMBL; AF035024; AAD56260.1; -; mRNA.  
DR PIR; S78486; S78486.  
DR HSSP; P01772; 2FB4.  
DR SMR; Q9UL90; 1-113.

DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
FT NON\_TER 1 113 113  
FT NON\_TER 113 113  
SQ SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07F CRC64;  
  
Query Match 76.9%; Score 513.5; DB 2; Length 113;  
Best Local Similarity 79.4%; Pred. No. 9e-44;  
Matches 100; Conservative 5; Mismatches 8; Indels 13; Gaps 1;  
  
QY 1 QVQLVESGGGVQPGKSLRLSCAASGFISSYAMHWVRQAPGNGLEWVAFMSYDGSNKKY 60  
Db 1 EVQLVESGGGVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIRYDGSNKKY 60  
  
QY 61 ADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDRGIAAGNYYYYGMDVWGQGT 120  
Db 61 ADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKD-----LNYWGQGT 107  
  
QY 121 TVTVSS 126  
Db 108 LVTVSS 113  
  
RESULT 7  
Q8WU38 HUMAN  
ID Q8WU38\_HUMAN PRELIMINARY; PRT; 573 AA.  
AC Q8WU38;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE IGH domain protein.  
DE GN Name=IGHD;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Primary B-Cells;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Udgin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";  
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Primary B-Cells;  
RA Director MGC Project;  
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP PROTEIN SEQUENCE.  
RX PubMed=1555592;  
RA Makiya R., Stigbrand T.;  
RT "Placental alkaline phosphatase has a binding site for the human



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RT      immunoglobulin-G Fc portion.";
RL      Eur. J. Biochem. 205:341-345(1992).
DR      EMBL; BC021276; AAH21276.1; -; mRNA.
DR      PIR; S21205; S21205.
DR      PIR; S30532; S30532.
DR      HSSP; P18529; I18K.
DR      Ensembl; ENSG00000196122; Homo sapiens.
DR      InterPro; IPR007110; Ig-like.
DR      InterPro; IPR003597; Ig_c1.
DR      InterPro; IPR003006; Ig_MHC.
DR      InterPro; IPR003596; Ig_v.
DR      Pfam; PF07654; C1-set; 1.
DR      Pfam; PF00047; ig; 2.
DR      SMART; SM00406; IGV; 1.
DR      PROSITE; PS50835; IG_LIKE; 4.
DR      PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW      Immunoglobulin domain; Repeat.
SQ      SEQUENCE 573 AA; 62967 MW; FD072344033AC530 CRC64;

      Query Match      76.3%; Score 510; DB 2; Length 573;
      Best Local Similarity 76.6%; Pred. No. 1.3e-42;
      Matches 98; Conservative 12; Mismatches 12; Indels 6; Gaps 2;

Qy      1 QVQLVESGGGVQPGRSRLSLSCAASGFIFSSYAMHWVRQAPGNGLEWVAFMSYDGSNKKY 60
Db      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
      20 EVQLVESGGGLVQPGRSRLSLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGISWNSIGY 79

Qy      61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDRGIAAGGNY--YYYGMDVWGQ 118
Db      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
      80 ADSVKGRFTISRDNKNSLYLQMNSLRAEDTALYYCAKH----GSGSYIGYYYGMDVWGQ 135

Qy      119 GTTVTVSS 126
Db      |||||

Qy      136 GTTVTVSS 143

RESULT 8
HV3G_HUMAN      STANDARD;      PRT;      122 AA.
AC      P01768;
DT      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DT      10-MAY-2005 (Rel. 47, Last annotation update)
DE      Ig heavy chain V-III region CAM.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC      Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      PROTEIN SEQUENCE.
RX      MEDLINE=81013859; PubMed=6774332;
RA      Lehman D.W., Putnam F.W.;
RT      "Amino acid sequence of the variable region of a human mu chain:
RT      location of a possible JH segment.";
RL      Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).
CC      -!- MISCELLANEOUS: This mu chain was isolated from the plasma of a
CC      patient with macroglobulinemia.
CC      -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC      -----
CC      This Swiss-Prot entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use as long as its content is in no way modified and this statement is not
CC      removed.
CC      -----
DR      PIR; A02051; M3HUAM.
DR      HSSP; P01772; 2FB4.
DR      SMR; P01768; 2-122.
DR      GO; GO:0005576; C:extracellular region; NAS.
DR      GO; GO:0003823; F:antigen binding; NAS.
DR      GO; GO:0006955; P:immune response; NAS.
DR      InterPro; IPR007110; Ig-like.
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DR      InterPro; IPR003596; Ig_v.
DR      SMART; SM00406; IGV; 1.
DR      PROSITE; PS50835; IG_LIKE; 1.
KW      Direct protein sequencing; Immunoglobulin domain;
KW      Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT      DOMAIN 1 112 Ig-like.
FT      MOD_RES 1 1 Pyrrolidone carboxylic acid.
FT      NON_TER 122 122
SQ      SEQUENCE 122 AA; 13668 MW; A42D0F17D252F1C2 CRC64;

      Query Match      75.9%; Score 507; DB 1; Length 122;
      Best Local Similarity 76.2%; Pred. No. 4.5e-43;
      Matches 96; Conservative 14; Mismatches 12; Indels 4; Gaps 2;

Qy      1 QVQLVESGGGVQPGRSRLSLSCAASGFIFSSYAMHWVRQAPGNGLEWVAFMSYDGSNKKY 60
Db      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
      1 QVELVESGGGVVZPGRSLRLSLSCAASGFTFSNYAMHWVRQPPGKGLEWVAVISYBGBKYY 60

Qy      61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDRGIAAGGNYYYGMDVWGQST 120
Db      |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
      61 ABSVKGRFTISRDBSKBTLYLQMNSLRAEBTAVYYCARDRPLY--GBYRAF--NYWGQST 116

Qy      121 TTVTVSS 126
Db      |||||

Qy      117 LVTVSS 122

RESULT 9
Q9Y509_HUMAN
ID      Q9Y509_HUMAN PRELIMINARY;      PRT;      147 AA.
AC      Q9Y509;
DT      01-NOV-1999 (TrEMBLrel. 12, Created)
DT      01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      VH3 protein (Fragment).
GN      Name=VH3;
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC      Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RX      MEDLINE=96071149; PubMed=7475288;
RA      Cao J., Vescio R.A., Rettig M.B., Hong C.H., Kim A., Lee J.C.,
RA      Lichtenstein A.K., Berenson J.R.;
RT      "A CD10-positive subset of malignant cells is identified in multiple
RT      myeloma using PCR with patient-specific immunoglobulin gene primers.";
RL      Leukemia 9:1948-1953(1995).
DR      EMBL; S80860; AAD14339.1; -; mRNA.
DR      HSSP; P01842; 1AQK.
DR      Ensembl; ENSG00000130076; Homo sapiens.
DR      GO; GO:0005887; C:integral to plasma membrane; NAS.
DR      GO; GO:0016066; P:cellular defense response (sensu Vertebrata); NAS.
DR      InterPro; IPR007110; Ig-like.
DR      InterPro; IPR003596; Ig_v.
DR      SMART; SM00406; IGV; 1.
DR      PROSITE; PS50835; IG_LIKE; 1.
FT      NON_TER 147 147
SQ      SEQUENCE 147 AA; 15768 MW; 8489FCAA7BC925C CRC64;

      Query Match      75.3%; Score 503; DB 2; Length 147;
      Best Local Similarity 76.2%; Pred. No. 1.4e-42;
      Matches 96; Conservative 7; Mismatches 23; Indels 0; Gaps 0;

Qy      1 QVQLVESGGGVQPGRSRLSLSCAASGFIFSSYAMHWVRQAPGNGLEWVAFMSYDGSNKKY 60
Db      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
      1 QVHLVESGGGVQPGKSLRLSCEASGFTFTYGMVSRQAPGKGLDWVALISYDGSYQY 60

Qy      61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDRGIAAGGNYYYGMDVWGQST 120
Db      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
      61 AGSVKGRFTISRDNKNTLYLQMTSLRVEDTAVYYCAKDNFYFDSVGYYYAGIDYWGQST 120
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FT	STRAND	68	73				
FT	TURN	74	77				
FT	STRAND	78	83				
FT	HELIX	88	90				
FT	STRAND	92	99				
FT	STRAND	106	106				
FT	TURN	107	108				
FT	STRAND	109	109				
FT	STRAND	113	116				
FT	STRAND	120	124				
SQ	SEQUENCE	126 AA; 13718 MW; E4D71B52B16F8776	CRC64;				
Query Match 73.8%; Score 493; DB 1; Length 126;							
Best Local Similarity 76.2%; Pred. NO. 1.2e-41;							
Matches 96; Conservative 11; Mismatches 19; Indels 0; Gaps 0;							
QY	1	QVQLVESGGVVQPGRSRLRLSCAASGFI	FSSYAMHWVRQAPGNGL	EWAFMSYDGSNKKY	60		
Db	1	QVQLVESGGVVQPGRSRLRLSCSSGFI	FSSYAMYVVRQAPGKLEWVAII	WDDGSDQHY	60		
QY	61	ADSVKGRFTISRDN	SKNTLYLQMN	SLRAEDTAVYYC	ARDRGIAAGNNYYYGMDVWGQGT	120	
Db	61	ADSVKGRFTISRDN	SKNTLFLQMD	SLRPEDTGVYFC	ARDGGHFCSSASC	FGPDYWGQGT	120
QY	121	TVTVSS	126				
Db	121	PVTVSS	126				
RESULT 12							
Q9UL84_HUMAN							
ID	Q9UL84_HUMAN	PRELIMINARY;	PRT;	122 AA.			
AC	Q9UL84;						
DT	01-MAY-2000	(TREMBLrel. 13, Created)					
DT	01-MAY-2000	(TREMBLrel. 13, Last sequence update)					
DT	01-OCT-2003	(TREMBLrel. 25, Last annotation update)					
DE	Myosin-reactive immunoglobulin heavy chain variable region (Fragment).						
DE							
OS	Homo sapiens (Human).						
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;						
OC	Homo.						
OX	NCBI_TaxID=9606;						
RN	[1]						
RP	NUCLEOTIDE SEQUENCE.						
RX	MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;						
RA	Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,						
RA	Young D.C.;						
RT	"Myosin-reactive autoantibodies in rheumatic carditis and normal fetus.";						
RT							
RRL	Clin. Immunol. Immunopathol. 87:184-192(1998).						
DR	EMBL; AF035030; AAD56266.1; -; mRNA.						
DR	HSSP; P01772; 2FB4.						
DR	SMR; Q9UL84; 1-122.						
DR	Ensembl; ENSG00000130076; Homo sapiens.						
DR	InterPro; IPR007110; Ig-like.						
DR	InterPro; IPR003596; Ig_v.						
DR	SMART; SM00406; IGV; 1.						
DR	PROSITE; PS50835; IG_LIKE; 1.						
FT	NON_TER	1	NON_TER	1			
FT	NON_TER	122	NON_TER	122			
SQ	SEQUENCE	122 AA; 13579 MW; 36054D41366545B8	CRC64;				
Query Match 72.6%; Score 485; DB 2; Length 122;							
Best Local Similarity 77.0%; Pred. NO. 7.3e-41;							
Matches 97; Conservative 6; Mismatches 19; Indels 4; Gaps 1;							
QY	1	QVQLVESGGVVQPGRSRLRLSCAASGFI	FSSYAMHWVRQAPGNGL	EWAFMSYDGSNKKY	60		
Db	1	EVQLVESGGVVQPGRSRLRLSCAASRFT	FSNYGMHWVRQAPGKLEWVA	AISNDGSNKKFY	60		
QY	61	ADSVKGRFTISRDN	SKNTLYLQMN	SLRAEDTAVYYC	ARDRGIAAGNNYYYGMDVWGQGT	120	
				:			

Db	61	ADSVKGRFTIFRDN	SKNMMDLQMN	SLRAEDTAVYYCAKDERGLVGTYF	-----DYWGQGT	116
QY	121	TVTVSS	126			
Db	117	LVTVSS	122			
RESULT 13						
ID	Q96BB9	HUMAN	PRELIMINARY;	PRT;	597 AA.	
AC	Q96BB9;					
DT	01-DEC-2001	(TREMBLrel. 19, Created)				
DT	01-DEC-2001	(TREMBLrel. 19, Last sequence update)				
DT	01-MAR-2004	(TREMBLrel. 26, Last annotation update)				
DE	IGHM protein.					
GN	Name=IGHM;					
OS	Homo sapiens (Human).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;					
OC	Homo.					
OX	NCBI_TaxID=9606;					
RN	[1]					
RP	NUCLEOTIDE SEQUENCE.					
RC	TISSUE=Primary B-Cells;					
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;					
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,					
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,					
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,					
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,					
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,					
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,					
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,					
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,					
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,					
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,					
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,					
RA	Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,					
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,					
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,					
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,					
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,					
RA	Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;					
RT	"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";					
RT	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).					
RL	[2]					
RN	NUCLEOTIDE SEQUENCE.					
RP	TISSUE=Primary B-Cells;					
RC	NIH MGC Project;					
RG	Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.					
RL	[3]					
RN	NUCLEOTIDE SEQUENCE.					
RP	PubMed=2500644;					
RX	Kishimoto T., Okajima H., Okumoto T., Taniguchi M.;					
RA	"Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-					
RT	chains Of a human monoclonal antibody with broad reactivity to					
RT	malignant tumor cells.";					
RL	Nucleic Acids Res. 17:4385-0(1989).					
DR	EMBL; BC015760; AAH15760.1; -; mRNA.					
DR	PIR; S05271; S05271.					
DR	PIR; S24260; S24260.					
DR	HSSP; P01861; 1ADQ.					
DR	Ensembl; ENSG00000130076; Homo sapiens.					
DR	InterPro; IPR007110; Ig-like.					
DR	InterPro; IPR003597; Ig cl.					
DR	InterPro; IPR003006; Ig_MHC.					
DR	InterPro; IPR003596; Ig_v.					
DR	Pfam; PF07654; C1-set; 4.					
DR	SMART; SM00406; IGV; 1.					
DR	PROSITE; PS50835; IG_LIKE; 5.					
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_3.					
KW	Immunoglobulin domain.					
SQ	SEQUENCE	597 AA; 65039 MW; 4FCA3AD8ECE263D9	CRC64;			



Db 1 QVZLVZSGGAVZPGRSLRLSCAASGFSFSTYAMHWVRQAPGKGLZWLSVISYBGBBZYY 60

QY 61 ADSVKGRFTISRDN SKNTLYLQWNSLRAEDTAVYYCARDRGIAAGNYYYYYGM DVWGQGT 120

Db 61 AASVKGRFTISRBB SKBTMYLEWNSLRAENTAVYYCARS-GIALGS---VAGTDYWGZGT 116

QY 121 TTVVSS 126

Db 117 LVTISS 122

Search completed: December 28, 2005, 14:03:08

Job time : 160.923 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 28, 2005, 13:53:15 ; Search time 35 Seconds  
(without alignments)  
297.632 Million cell updates/sec

Title: US-09-920-137F-7  
Perfect score: 668  
Sequence: 1 QQLVESGGGVQPGKSLRL.....NYYYGMVDVWGQTTVTSS 126

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/iaa/6\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/H\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/RE\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	572.5	85.7	451	2	US-09-472-087-70	Sequence 70, Appl
2	565	84.6	126	2	US-09-240-274-26	Sequence 26, Appl
3	565	84.6	126	2	US-09-848-798-26	Sequence 26, Appl
4	559	83.7	126	2	US-09-240-274-153	Sequence 153, App
5	559	83.7	126	2	US-09-848-798-153	Sequence 153, App
6	557	83.4	126	2	US-09-240-274-25	Sequence 25, Appl
7	557	83.4	126	2	US-09-848-798-25	Sequence 25, Appl
8	554	82.9	310	2	US-09-079-029-11	Sequence 11, Appl
9	548.5	82.1	125	2	US-09-240-274-140	Sequence 140, App
10	548.5	82.1	125	2	US-09-848-798-140	Sequence 140, App
11	546	81.7	120	2	US-10-330-613A-29	Sequence 29, Appl
12	541.5	81.1	123	2	US-09-424-840B-6	Sequence 6, Appl1
13	538	80.5	126	2	US-09-240-274-13	Sequence 13, Appl
14	538	80.5	126	2	US-09-848-798-13	Sequence 13, Appl
15	537	80.4	124	2	US-09-424-840B-16	Sequence 16, Appl
16	537	80.4	126	2	US-09-240-274-152	Sequence 152, App
17	537	80.4	126	2	US-09-848-798-152	Sequence 152, App
18	536	80.2	126	2	US-09-240-274-146	Sequence 146, App
19	536	80.2	126	2	US-09-848-798-146	Sequence 146, App
20	535	80.1	126	2	US-09-240-274-17	Sequence 17, Appl
21	535	80.1	126	2	US-09-848-798-17	Sequence 17, Appl
22	533	79.8	123	2	US-08-983-607-38	Sequence 38, Appl
23	530.5	79.4	119	1	US-08-331-398A-46	Sequence 46, Appl
24	530.5	79.4	119	1	US-08-331-397B-46	Sequence 46, Appl
25	530.5	79.4	119	1	US-08-759-804A-46	Sequence 46, Appl
26	530.5	79.4	119	2	US-09-227-693-46	Sequence 46, Appl
27	530.5	79.4	120	1	US-07-942-245-35	Sequence 35, Appl

28	529.5	79.3	167	2	US-09-472-087-80	Sequence 80, Appl
29	529.5	79.3	287	2	US-08-862-124-17	Sequence 17, Appl
30	529.5	79.3	304	2	US-08-862-124-14	Sequence 14, Appl
31	528.5	79.1	115	2	US-09-269-332-89	Sequence 89, Appl
32	526.5	78.8	123	2	US-09-560-198A-2	Sequence 2, Appl1
33	526.5	78.8	127	2	US-09-240-274-139	Sequence 139, App
34	526.5	78.8	127	2	US-09-848-798-139	Sequence 139, App
35	525	78.6	128	2	US-09-840-459-77	Sequence 77, Appl
36	525	78.6	128	2	US-09-840-459-79	Sequence 79, Appl
37	525	78.6	128	2	US-09-497-625A-77	Sequence 77, Appl
38	525	78.6	128	2	US-09-497-625A-79	Sequence 79, Appl
39	524	78.4	248	2	US-09-315-926A-80	Sequence 80, Appl
40	522.5	78.2	127	2	US-09-240-274-145	Sequence 145, App
41	522.5	78.2	127	2	US-09-848-798-145	Sequence 145, App
42	522	78.1	126	2	US-09-240-274-16	Sequence 16, Appl
43	522	78.1	126	2	US-09-848-798-16	Sequence 16, Appl
44	520	77.8	128	2	US-09-240-274-1	Sequence 1, Appli
45	520	77.8	128	2	US-09-848-798-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1  
US-09-472-087-70  
; Sequence 70, Application US/09472087  
; Patent No. 6682736  
; GENERAL INFORMATION:  
; APPLICANT: HANSON, DOUGLAS C.  
; APPLICANT: NEVEU, MARK J.  
; APPLICANT: MUELLER, EILLEN E.  
; APPLICANT: HANKE, JEFFREY H.  
; APPLICANT: GILMAN, STEVEN C.  
; APPLICANT: DAVIS, C. GEOFFREY  
; APPLICANT: CORVALAN, JOSE R.  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4  
; FILE REFERENCE: ABX-PF1  
; CURRENT APPLICATION NUMBER: US/09/472,087  
; CURRENT FILING DATE: 1999-12-23  
; PRIOR APPLICATION NUMBER: 60/113,647  
; PRIOR FILING DATE: 1998-12-23  
; NUMBER OF SEQ ID NOS: 147  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 70  
; LENGTH: 451  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-472-087-70

Query Match 85.7%; Score 572.5; DB 2; Length 451;  
Best Local Similarity 89.8%; Pred. No. 8.1e-49;  
Matches 114; Conservative 1; Mismatches 9; Indels 3; Gaps 2;

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Qy	61	ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYICARD-RGIAAGGNYYYYGMDVWGQ 119	
Db	61	ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYICARDPRG--ATLYYYGMDVWGQ 118	
Qy	120	TTVTVSS 126	
Db	119	TTVTVSS 125	

RESULT 2  
US-09-240-274-26  
; Sequence 26, Application US/09240274  
; Patent No. 6255455  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Donald L.  
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL

```

; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;
; FILE REFERENCE: 09596-42U2
;
; CURRENT APPLICATION NUMBER: US/09/240,274
;
; CURRENT FILING DATE: 1999-01-29
;
; EARLIER APPLICATION NUMBER: 60/081,380
;
; EARLIER FILING DATE: 1998-04-10
;
; EARLIER APPLICATION NUMBER: 60/028,550
;
; EARLIER FILING DATE: 1996-10-11
;
; NUMBER OF SEQ ID NOS: 224
;
; SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 26
;
; LENGTH: 126
;
; TYPE: PRT
;
; ORGANISM: Homo sapiens
;
; FEATURE:
;
; OTHER INFORMATION: anti-Rh(D) chain D31
;
US-09-240-274-26

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Query Match	84.6%;	Score 565;	DB 2;	Length 126;
Best Local Similarity	84.1%;	Pred. No. 1e-48;		
Matches 106;	Conservative	8;	Mismatches 12;	Indels 0; Gaps 0;
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		:   :		:
Db	1	EVQLLESGGGVVQ	PGSLRLSCAASGFT	FSSYGMHWVRQAPGKLEWVAVVYDGSNKHY 60
		:   :		:
Qy	61	ADSVKGRFTISR	DNKNTLYLQMN	SLRAEDTAVYYCARDRGIAAGCNYYYGYMDVWGQGT 120
		:		:
Db	61	SDSVKGRFTISR	DNKNTLYLQMD	SLRAEDTAVYYCARERNFRSGYSRYGYMDVWGPGT 120
Qy	121	TVT	VSS 126	
Db	121	TVT	VSS 126	

RESULT 3  
 US-09-848-798-26  
 ; Sequence 26, Application US/09848798  
 ; Patent No. 6858719  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Siegel, Donald L.  
 ; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
 ; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF  
 ; FILE REFERENCE: 09596-42U2  
 ; CURRENT APPLICATION NUMBER: US/09/848,798  
 ; CURRENT FILING DATE: 2001-05-04  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11  
 ; NUMBER OF SEQ ID NOS: 224  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 26  
 ; LENGTH: 126  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; OTHER INFORMATION: anti-Rh(D) chain D31  
 ; US-09-848-798-26

	Query Match	84.6%;	Score 565;	DB 2;	Length 126;	
	Best Local Similarity	84.1%;	Pred. NO. 1e-48;			
	Matches 106;	Conservative	8;	Mismatches 12;	Indels	Gaps 0;
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Dd	1	EVQLLESGGGVVQPGRSRLRSCAASGFT	FSSYGMHWVRQAPGKGL	EWAFAFMSYDGSNKKY	60	
		: :: : :	:	:	:	:
Qy	61	ADSVKGRFTISRDNKNTLYLQMNSLR	AEDTAVVYCARDRIAAGGN	YYYGYMDVWGQT	120	
		: :: : :	:	:	:	:
Dd	61	SDSVKGRFTISRDNKNTLYLQMNSLR	AEDTAVVYCARERNFRSGYSR	YYYGYMDVWGPGT	120	
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Qy	121	TVTVSS	126			

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Db      121 TTVVSS 126
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RESULT 4
US-09-240-274-153
; Sequence 153, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 153
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH56
US-09-240-274-153

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Query Match	83.7%;	Score 559;	DB 2;	Length 126;
Best Local Similarity	83.3%;	Pred. No. 4.1e-48;		
Matches 105;	Conservative	8;	Mismatches 13;	Indels 0; Gaps 0;
Qy	1	QVQLVESGGGVQPGKSLRLSCAASGFISSYAMHWVRQAPGNGLEWVAFMSYDGSNKKY	60	
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Db	1	EVQLLESGGGVQPGKSLRLSCAASGFTFSSYGMHWVRQAPGKLEWVAVVYDGSNKHY	60	
		:   :		:
Qy	61	ADSVKGRFTTISRDN SKNTLYLQMNSLRAEDTAVYICARDRGIAAGNYYYYGMDVWGQT	120	
		:		:
Db	61	SDSVKGRFTTIFRDN SKNTLYLQMDSLRAEDTAVYICARENFRSGYSRYYYGMDVWGPGT	120	
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Qy	121	TVTIVSS	126	
Db	121	TVTIVSS	126	

RESULT 5  
 US-09-848-798-153  
 ; Sequence 153, Application US/09848798  
 ; Patent No. 6858719  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Siegel, Donald L.  
 ; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTI  
 ; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF  
 ; FILE REFERENCE: 09596-42U2  
 ; CURRENT APPLICATION NUMBER: US/09/848,798  
 ; CURRENT FILING DATE: 2001-05-04  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11  
 ; NUMBER OF SEQ ID NOS: 224  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 153  
 ; LENGTH: 126  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; OTHER INFORMATION: anti-Rh(D) antibody clone SH56  
 US-09-848-798-153

Query Match 83.7%; Score 559; DB 2; Length 126;  
Best Local Similarity 83.3%; Pred. No. 4.1e-48;







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; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: DE 19723904.8
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-424-840B-6

Query Match      81.1%; Score 541.5; DB 2; Length 123;
Best Local Similarity 84.1%; Pred. No. 2.2e-46;
Matches 106; Conservative 6; Mismatches 11; Indels 3; Gaps 1;

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Db      1 QVKLLESGGGVQPGKSLRLSCAASGFTFSSYAMHWVRQAPGKLEWVAVISYDGSNKYY 60
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY      61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDRGIAAGNYYYYGMDVWGQGT 120
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 ADSVKGRFAISRDNKNTLYLQMNSLRAEDTAVYYCARALGSWGGWDHY---MDVWGKGT 117
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY      121 TTVTVSS 126
      :|||||
Db      118 TTVTVSS 123
      :|||||

RESULT 13
US-09-240-274-13
; Sequence 13, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; EARLIER FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain D08
US-09-240-274-13

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Best Local Similarity 82.7%; Pred. No. 4.9e-46;
Matches 105; Conservative 9; Mismatches 11; Indels 2; Gaps 2;

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      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 EVQLLESGGGVQPGKSLRLSCAASGFTFSSYGMHWVRQAPGRGLEWVALIWYDGNKE 60
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY      60 YADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDRGIAAGNYYYYGMDVWGQ 119
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 YADSVKGRFISRDNKNTLYLQVNSLRADDTAVYYCARDQR-AAAGIFYYSRMDVWGQ 119
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QY      120 TTVTVSS 126
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Db      120 TTVTVSS 126
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RESULT 14
US-09-848-798-13
; Sequence 13, Application US/09848798
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; Patent No. 6858719
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain D08
US-09-848-798-13

Query Match      80.5%; Score 538; DB 2; Length 126;
Best Local Similarity 82.7%; Pred. No. 4.9e-46;
Matches 105; Conservative 9; Mismatches 11; Indels 2; Gaps 2;

QY      1 QVQLV-ESGGGVQPGKSLRLSCAASGIFSSYAMHWVRQAPGNGLEWVAFMSYDGSNKK 59
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 EVQLLESGGGVQPGKSLRLSCAASGFTFSSYGMHWVRQAPGRGLEWVALIWYDGNKE 60
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY      60 YADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDRGIAAGNYYYYGMDVWGQ 119
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 YADSVKGRFISRDNKNTLYLQVNSLRADDTAVYYCARDQR-AAAGIFYYSRMDVWGQ 119
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY      120 TTVTVSS 126
      :|||||
Db      120 TTVTVSS 126
      :|||||

RESULT 15
US-09-424-840B-16
; Sequence 16, Application US/09424840B
; Patent No. 6790938
; GENERAL INFORMATION:
; APPLICANT: Berchtold, Peter
; APPLICANT: Escher, Robert F. A.
; TITLE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES
; FILE REFERENCE: 100564-09049
; CURRENT APPLICATION NUMBER: US/09/424,840B
; CURRENT FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: DE 19820663.1
; PRIOR FILING DATE: 1998-05-08
; PRIOR APPLICATION NUMBER: DE 19755227.7
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: DE 19723904.8
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-424-840B-16

Query Match      80.4%; Score 537; DB 2; Length 124;
Best Local Similarity 82.7%; Pred. No. 6.1e-46;
Matches 105; Conservative 6; Mismatches 12; Indels 4; Gaps 2;

QY      1 QVQLVESGGGVQPGKSLRLSCAASGIFSSYAMHWVRQAPGNGLEWVAFMSYDGSNKKY 60
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 QVKLLESGGGVQPGKSLRLSCAASGFTFSSYTMHWVRQAPGKLEWVALISYDGSNKYY 60
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY      61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDRGIAAGNYYYY-GMDVWGQ 119
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 28, 2005, 14:03:21 ; Search time 119.538 Seconds  
(without alignments)  
440.415 Million cell updates/sec

Title: US-09-920-137F-7  
Perfect score: 668  
Sequence: 1 QVQLVESGGGVQPGKSLRL.....NYYYGMDVWGQGTITVTVSS 126

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA Main:\*  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	584.5	87.5	123	4	US-10-292-088-117 Sequence 117, App
2	584.5	87.5	138	4	US-10-325-694-144 Sequence 144, App
3	583	87.3	135	4	US-10-364-743-14 Sequence 14, Appl
4	583	87.3	135	4	US-10-364-743-98 Sequence 98, Appl
5	583	87.3	135	5	US-10-452-593-14 Sequence 14, Appl
6	583	87.3	135	5	US-10-452-593-98 Sequence 98, Appl
7	582	87.1	124	4	US-10-371-942-82 Sequence 82, Appl
8	581.5	87.1	138	4	US-10-325-694-150 Sequence 150, App
9	581.5	87.1	457	5	US-10-778-915-1 Sequence 1, Appli
10	581	87.0	126	4	US-10-041-860-17 Sequence 17, Appl
11	581	87.0	126	4	US-10-041-860-209 Sequence 209, App
12	581	87.0	126	4	US-10-041-860-282 Sequence 282, App
13	581	87.0	126	4	US-10-665-383-14 Sequence 14, Appl
14	580.5	86.9	123	4	US-10-292-088-116 Sequence 116, App
15	579	86.7	124	4	US-10-292-088-106 Sequence 106, App
16	579	86.7	126	4	US-10-041-860-25 Sequence 25, Appl
17	579	86.7	126	4	US-10-041-860-210 Sequence 210, App
18	579	86.7	126	4	US-10-041-860-246 Sequence 246, App
19	579	86.7	126	4	US-10-041-860-306 Sequence 306, App
20	579	86.7	126	4	US-10-665-383-30 Sequence 30, Appl
21	579	86.7	126	5	US-10-727-155-128 Sequence 128, App
22	578.5	86.6	125	4	US-10-292-088-107 Sequence 107, App
23	577.5	86.5	123	4	US-10-292-088-115 Sequence 115, App
24	577.5	86.5	125	5	US-10-727-155-222 Sequence 222, App
25	577	86.4	115	4	US-10-305-347A-7 Sequence 7, Appli
26	577	86.4	115	5	US-10-954-900A-7 Sequence 7, Appli
27	577	86.4	141	5	US-10-858-855-11 Sequence 11, Appl

28	575.5	86.2	125	5	US-10-727-155-206 Sequence 206, App
29	575.5	86.2	125	5	US-10-727-155-218 Sequence 218, App
30	573	85.8	134	5	US-10-727-155-254 Sequence 254, App
31	572.5	85.7	252	3	US-09-880-748-1731 Sequence 1731, Ap
32	572.5	85.7	252	4	US-10-293-418-1731 Sequence 1731, Ap
33	572.5	85.7	451	4	US-10-153-382-17 Sequence 17, Appl
34	572.5	85.7	451	5	US-10-612-497-70 Sequence 70, Appl
35	572.5	85.7	451	5	US-10-776-649-70 Sequence 70, Appl
36	572.5	85.7	451	6	US-11-085-368-17 Sequence 17, Appl
37	572	85.6	122	5	US-10-727-155-34 Sequence 34, Appl
38	572	85.6	126	4	US-10-041-860-245 Sequence 245, App
39	571.5	85.6	123	4	US-10-269-711-11 Sequence 11, Appl
40	571.5	85.6	123	4	US-10-269-711-23 Sequence 23, Appl
41	571.5	85.6	123	4	US-10-269-711-27 Sequence 27, Appl
42	571.5	85.6	123	4	US-10-269-711-31 Sequence 31, Appl
43	571.5	85.6	123	4	US-10-269-711-35 Sequence 35, Appl
44	571.5	85.6	123	4	US-10-684-109-11 Sequence 11, Appl
45	571	85.5	135	4	US-10-364-743-95 Sequence 95, Appl

ALIGNMENTS

RESULT 1  
US-10-292-088-117  
; Sequence 117, Application US/10292088  
; Publication No. US20030211100A1  
; GENERAL INFORMATION:  
; APPLICANT: BEDIAN, VAHE  
; APPLICANT: GLADUE, RONALD P.  
; APPLICANT: CORVALAN, JOSE  
; APPLICANT: JIA, XIAO-CHI  
; APPLICANT: FENG, XIAO  
; TITLE OF INVENTION: ANTIBODIES TO CD40  
; FILE REFERENCE: ABX-PF/3 US  
; CURRENT APPLICATION NUMBER: US/10/292,088  
; CURRENT FILING DATE: 2003-03-14  
; PRIOR APPLICATION NUMBER: 60/348,980  
; PRIOR FILING DATE: 2001-11-09  
; NUMBER OF SEQ ID NOS: 147  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 117  
; LENGTH: 123  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-292-088-117

Query Match	87.5%;	Score 584.5;	DB 4;	Length 123;
Best Local Similarity	90.5%;	Pred. No. 3.1e-48;		
Matches 114;	Conservative 1;	Mismatches 8;	Indels 3;	Gaps 1;
Qy	1	QVQLVESGGGVQPGKSLRLSCAASGFISSYAMHWVRQAPGNGLEWVAFMSYDGSNKKY 60		
Db	1	QVQLVESGGGVQPGKSLRLSCAASGFTSSYAMHWVRQAPGKLEWVAVISYDGSNKYY 60		
Qy	61	ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDRGIAAGNNYYYGMDVWGQGT 120		
Db	61	ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDYG---DYYYYYGMDVWGQGT 117		
Qy	121	TVTSS 126		
Db	118	TVTSS 123		

RESULT 2  
US-10-325-694-144  
; Sequence 144, Application US/10325694  
; Publication No. US20030148463A1  
; GENERAL INFORMATION:  
; APPLICANT: KUFER, PETER  
; APPLICANT: RAUM, TOBIAS  
; TITLE OF INVENTION: NOVEL METHOD FOR THE PRODUCTION OF ANTI-HUMAN ANTIGEN  
; TITLE OF INVENTION: RECEPTORS AND USES THEREOF



```

; FILE REFERENCE: 38164000
; CURRENT APPLICATION NUMBER: US/10/325,694
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US/09/403,107
; PRIOR FILING DATE: 1999-10-14
; NUMBER OF SEQ ID NOS: 152
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 144
; LENGTH: 138
; TYPE: PRT
; ORGANISM: HUMAN
US-10-325-694-144

Query Match      87.5%; Score 584.5; DB 4; Length 138;
Best Local Similarity 88.2%; Pred. No. 3.5e-48;
Matches 112; Conservative 4; Mismatches 10; Indels 1; Gaps 1;

QY      1 QVQLVESGGGVQPGRSLRLSCAASGFISSYAMHWVRQAPGNGLEWVAFMSYDGSNKKY 60
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 EVQLVESGGGVQPGRSLRLSCAASGFTFSSYGHVWRQAPGKGLEWVAVISYDGSNKKY 60

QY      61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDRGIAAGN-YYYYGMDVWGQ 119
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKDMGWGSGWRPYYYYGMDVWGQ 120

QY      120 TTVTVSS 126
      |||||
Db      121 TTVTVSS 127

RESULT 3
US-10-364-743-14
; Sequence 14, Application US/10364743
; Publication No. US20040009178A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Wild, Martha A.
; APPLICANT: Maruyama, Toshiaki
; APPLICANT: No. US20040009178Alan, Mary Jean
; TITLE OF INVENTION: IMMUNOTHERAPEUTICS FOR BIODEFENSE
; FILE REFERENCE: 84 (1087-73)
; CURRENT APPLICATION NUMBER: US/10/364,743
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: US 60/428,807
; PRIOR FILING DATE: 2002-11-25
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 135
; TYPE: PRT
; ORGANISM: human
; NAME/KEY: MISC FEATURE
; LOCATION: (26)..(26)
; OTHER INFORMATION: xaa=unknown amino acid
US-10-364-743-14

Query Match      87.3%; Score 583; DB 4; Length 135;
Best Local Similarity 86.7%; Pred. No. 4.8e-48;
Matches 111; Conservative 4; Mismatches 11; Indels 2; Gaps 1;

QY      1 QVQLVESGGGVQPGRSLRLSCAASGFISSYAMHWVRQAPGNGLEWVAFMSYDGSNKKY 60
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      3 EVQLVESGGGVQPGRSLRLSCAXSGFIFSSYGLHWVRQAPGKGLEWVAFISYDGSKKY 62

QY      61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDRGIAAGN--YYYYGMDVWGQ 118
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      63 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKDRVIVPAANKYYYYYGMVDVWGQ 122

QY      119 GTTVTVSS 126
      |||||
Db      123 GTTVTVSS 130

Query Match      87.3%; Score 583; DB 4; Length 135;
Best Local Similarity 86.7%; Pred. No. 4.8e-48;
Matches 111; Conservative 4; Mismatches 11; Indels 2; Gaps 1;

QY      1 QVQLVESGGGVQPGRSLRLSCAASGFISSYAMHWVRQAPGNGLEWVAFMSYDGSNKKY 60
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      3 EVQLVESGGGVQPGRSLRLSCAXSGFIFSSYGLHWVRQAPGKGLEWVAFISYDGSKKY 62

QY      61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDRGIAAGN--YYYYGMDVWGQ 118
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      63 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKDRVIVPAANKYYYYYGMVDVWGQ 122

QY      119 GTTVTVSS 126
      |||||
Db      123 GTTVTVSS 130
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```

RESULT 4
US-10-364-743-98
; Sequence 98, Application US/10364743
; Publication No. US20040009178A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Wild, Martha A.
; APPLICANT: Maruyama, Toshiaki
; APPLICANT: No. US20040009178Alan, Mary Jean
; TITLE OF INVENTION: IMMUNOTHERAPEUTICS FOR BIODEFENSE
; FILE REFERENCE: 84 (1087-73)
; CURRENT APPLICATION NUMBER: US/10/364,743
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: US 60/428,807
; PRIOR FILING DATE: 2002-11-25
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 98
; LENGTH: 135
; TYPE: PRT
; ORGANISM: human
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (26)..(26)
; OTHER INFORMATION: xaa=unknown amino acid
US-10-364-743-98

Query Match      87.3%; Score 583; DB 4; Length 135;
Best Local Similarity 86.7%; Pred. No. 4.8e-48;
Matches 111; Conservative 4; Mismatches 11; Indels 2; Gaps 1;

QY      1 QVQLVESGGGVQPGRSLRLSCAASGFISSYAMHWVRQAPGNGLEWVAFMSYDGSNKKY 60
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      3 EVQLVESGGGVQPGRSLRLSCAXSGFIFSSYGLHWVRQAPGKGLEWVAFISYDGSKKY 62

QY      61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDRGIAAGN--YYYYGMDVWGQ 118
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      63 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKDRVIVPAANKYYYYYGMVDVWGQ 122

QY      119 GTTVTVSS 126
      |||||
Db      123 GTTVTVSS 130

RESULT 5
US-10-452-593-14
; Sequence 14, Application US/10452593
; Publication No. US20040258699A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Wild, Martha A.
; APPLICANT: Maruyama, Toshiaki
; APPLICANT: Nolan, Mary Jean
; TITLE OF INVENTION: IMMUNOTHERAPEUTICS FOR BIODEFENSE
; FILE REFERENCE: 98 CIP (1087-73 CIP)
; CURRENT APPLICATION NUMBER: US/10/452,593
; CURRENT FILING DATE: 2003-06-02
; PRIOR APPLICATION NUMBER: US 10/364,743
; PRIOR FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: US 60/356,086
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/376,408
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: US 60/428,807
; PRIOR FILING DATE: 2002-11-25
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 135
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; TYPE: PRT
; ORGANISM: human
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (26)..(26)
; OTHER INFORMATION: xaa=unknown amino acid
US-10-452-593-14

Query Match      87.3%; Score 583; DB 5; Length 135;
Best Local Similarity 86.7%; Pred. No. 4.8e-48;
Matches 111; Conservative 4; Mismatches 11; Indels 2; Gaps 1;

Qy      1 QVQLVESGGGVQPGRSLRLSCAASGFIPISSYAMHWVRQAPGNGLEWVAFMYSYDGSNKKY 60
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      3 EVQLVESGGGVQPGRSLRLSCAXSGFIPISSYGLHWVRQAPGKGLEWVAFISYDGSKNY 62

Qy      61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCARDRGIAAGN--YYTYGMDVMGQ 118
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      63 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKDRVIVPAANKYYYYYGMVWGQ 122

Qy      119 GTTVTVSS 126
      |||||
Db      123 GTTVTVSS 130

RESULT 6
US-10-452-593-98
; Sequence 98, Application US/10452593
; Publication No. US20040258699A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Wild, Martha A.
; APPLICANT: Maruyama, Toshiaki
; APPLICANT: Nolan, Mary Jean
; TITLE OF INVENTION: IMMUNOTHERAPEUTICS FOR BIODEFENSE
; FILE REFERENCE: 98 CIP (1087-73 CIP)
; CURRENT APPLICATION NUMBER: US/10/452,593
; CURRENT FILING DATE: 2003-06-02
; PRIOR APPLICATION NUMBER: US 10/364,743
; PRIOR FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: US 60/356,086
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/376,408
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: US 60/428,807
; PRIOR FILING DATE: 2002-11-25
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 98
; LENGTH: 135
; TYPE: PRT
; ORGANISM: human
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (26)..(26)
; OTHER INFORMATION: xaa=unknown amino acid
US-10-452-593-98

Query Match      87.3%; Score 583; DB 5; Length 135;
Best Local Similarity 86.7%; Pred. No. 4.8e-48;
Matches 111; Conservative 4; Mismatches 11; Indels 2; Gaps 1;

Qy      1 QVQLVESGGGVQPGRSLRLSCAASGFIPISSYAMHWVRQAPGNGLEWVAFMYSYDGSNKKY 60
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      3 EVQLVESGGGVQPGRSLRLSCAXSGFIPISSYGLHWVRQAPGKGLEWVAFISYDGSKNY 62

Qy      61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCARDRGIAAGN--YYTYGMDVMGQ 118
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      63 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKDRVIVPAANKYYYYYGMVWGQ 122

Qy      119 GTTVTVSS 126
      |||||
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```
Db      123 GTTVTVSS 130

RESULT 7
US-10-371-942-82
; Sequence 82, Application US/10371942
; Publication No. US20030223994A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Henricus Renerus Jacobus Mattheus
; APPLICANT: Reiter, Yoram
; TITLE OF INVENTION: MHC-PEPTIDE COMPLEX BINDING LIGANDS
; FILE REFERENCE: 10280-034001
; CURRENT APPLICATION NUMBER: US/10/371,942
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,994
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 82
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-371-942-82

Query Match      87.1%; Score 582; DB 4; Length 124;
Best Local Similarity 88.9%; Pred. No. 5.5e-48;
Matches 112; Conservative 3; Mismatches 9; Indels 2; Gaps 1;

Qy      1 QVQLVESGGGVQPGRSLRLSCAASGFIPISSYAMHWVRQAPGNGLEWVAFMYSYDGSNKKY 60
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      1 QVQLVQSGGGVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKY 60

Qy      61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCARDRGIAAGNYYYGMVWGQT 120
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCARD--FDYGDSYYYYYGMVWGQT 118

Qy      121 TTVTVSS 126
      |||||
Db      119 TTVTVSS 124

RESULT 8
US-10-325-694-150
; Sequence 150, Application US/10325694
; Publication No. US20030148463A1
; GENERAL INFORMATION:
; APPLICANT: KUFER, PETER
; APPLICANT: RAUM, TOBIAS
; TITLE OF INVENTION: NOVEL METHOD FOR THE PRODUCTION OF ANTI-HUMAN ANTIGEN
; TITLE OF INVENTION: RECEPTORS AND USES THEREOF
; FILE REFERENCE: 38164000
; CURRENT APPLICATION NUMBER: US/10/325,694
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US/09/403,107
; PRIOR FILING DATE: 1999-10-14
; NUMBER OF SEQ ID NOS: 152
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 150
; LENGTH: 138
; TYPE: PRT
; ORGANISM: HUMAN
US-10-325-694-150

Query Match      87.1%; Score 581.5; DB 4; Length 138;
Best Local Similarity 87.4%; Pred. No. 6.8e-48;
Matches 111; Conservative 5; Mismatches 10; Indels 1; Gaps 1;

Qy      1 QVQLVESGGGVQPGRSLRLSCAASGFIPISSYAMHWVRQAPGNGLEWVAFMYSYDGSNKKY 60
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      1 EVQLLESGGGVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKY 60

Qy      61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCARDRGIAAGN--YYTYGMDVMGQ 119
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```



```
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 282
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-282

Query Match      87.0%; Score 581; DB 4; Length 126;
Best Local Similarity 88.1%; Pred. No. 6.9e-48;
Matches 111; Conservative 3; Mismatches 12; Indels 0; Gaps 0;

QY      1 QVQLVESGGGVQPGKSLRLSCAASGFIFFSSYAMHWVRQAPGNGLEWVAFMSYDGSNKYY 60
Db      1 QVQLVESGGGVQPGKSLRLSCAASGFTFSSYGMHWVRQAPGKLEWAVIWDGSNKYY 60

QY      61 ADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDRGIAAGNYYYGMDVWGQGT 120
Db      61 ADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDQGYRYAGYYDYGMVWGQGT 120

QY      121 TTVTVSS 126
Db      121 TTVTVSS 126

RESULT 13
US-10-665-383-14
; Sequence 14, Application US/10665383
; Publication No. US20040141969A1
; GENERAL INFORMATION:
; APPLICANT: Floege, Juergen
; APPLICANT: Gazit, Gadi
; APPLICANT: Keyt, Bruce
; APPLICANT: LaRochelelle, William
; APPLICANT: Lichenstein, Henri
; TITLE OF INVENTION: METHOD FOR THE TREATMENT OF NEPHRITIS
; TITLE OF INVENTION: USING ANTI-PDGF-DD ANTIBODIES
; FILE REFERENCE: ABGENIX.052A
; CURRENT APPLICATION NUMBER: US/10/665,383
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: 60/411,137
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-665-383-14

Query Match      87.0%; Score 581; DB 4; Length 126;
Best Local Similarity 88.1%; Pred. No. 6.9e-48;
Matches 111; Conservative 3; Mismatches 12; Indels 0; Gaps 0;

QY      1 QVQLVESGGGVQPGKSLRLSCAASGFIFFSSYAMHWVRQAPGNGLEWVAFMSYDGSNKYY 60
Db      1 QVQLVESGGGVQPGKSLRLSCAASGFTFSSYGMHWVRQAPGKLEWAVIWDGSNKYY 60

QY      61 ADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDRGIAAGNYYYGMDVWGQGT 120
Db      61 ADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDQGYRYAGYYDYGMVWGQGT 120

QY      121 TTVTVSS 126
Db      121 TTVTVSS 126
```

```
US-10-292-088-116
; Sequence 116, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 116
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-116

Query Match      86.9%; Score 580.5; DB 4; Length 123;
Best Local Similarity 89.7%; Pred. No. 7.5e-48;
Matches 113; Conservative 1; Mismatches 9; Indels 3; Gaps 1;

QY      1 QVQLVESGGGVQPGKSLRLSCAASGFIFFSSYAMHWVRQAPGNGLEWVAFMSYDGSNKYY 60
Db      1 QVQLVESGGGVQPGKSLRLSCAASGFTFSSYGMHWVRQAPGKLEWAVIWDGSNKYY 60

QY      61 ADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDRGIAAGNYYYGMDVWGQGT 120
Db      61 ADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDYDGYG---DYDDYGGMDVWGQGT 117

QY      121 TTVTVSS 126
Db      118 TTVTVSS 123

RESULT 15
US-10-292-088-106
; Sequence 106, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 106
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-106

Query Match      86.7%; Score 579; DB 4; Length 124;
Best Local Similarity 88.9%; Pred. No. 1.1e-47;
Matches 112; Conservative 2; Mismatches 10; Indels 2; Gaps 1;

QY      1 QVQLVESGGGVQPGKSLRLSCAASGFIFFSSYAMHWVRQAPGNGLEWVAFMSYDGSNKYY 60
Db      1 QVQLVESGGGVQPGKSLRLSCAASGFTFSSYGMHWVRQAPGKLEWAVIWDGSNKYY 60

QY      61 ADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDRGIAAGNYYYGMDVWGQGT 120
```



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 28, 2005, 13:43:04 ; Search time 126.462 Seconds  
(without alignments)  
375.236 Million cell updates/sec

Title: US-09-920-137F-8  
Perfect score: 568  
Sequence: 1 EIVLTQSPATLSLSPGERAT.....QQRSNWPPFTFGPGTKVDIK 108

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_21:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	559	98.4	108	5 AAM51165	Aam51165 Anti-tumo
2	559	98.4	108	5 AAM51173	Aam51173 Human Vg/
3	559	98.4	108	5 AAU76334	Aau76334 Human ant
4	559	98.4	108	7 ADJ73533	Adj73533 Erythropro
5	559	98.4	108	7 ADJ73534	Adj73534 Erythropro
6	559	98.4	108	9 ADW07091	Adw07091 Anti-Psaa
7	559	98.4	129	5 AAM51174	Aam51174 Human rec
8	559	98.4	129	5 AAM51175	Aam51175 Human mAb
9	541	95.2	108	4 AAB72884	Aab72884 Human ant
10	541	95.2	108	9 AEB01062	Aeb01062 Human IP1
11	541	95.2	109	7 ADF11411	Adf11411 16E1 anti
12	541	95.2	215	7 ADF11435	Adf11435 16E1 anti
13	540	95.1	128	8 ADM41547	Adm41547 Anti-inte
14	540	95.1	130	7 ADD89877	Add89877 Human ant
15	540	95.1	130	8 ADS64664	Ads64664 Human 9E7
16	540	95.1	130	8 ADS64653	Ads64653 Human ant
17	540	95.1	235	8 ADM41573	Adm41573 Anti-inte
18	539	94.9	109	7 ADF11395	Adf11395 22B3 anti
19	539	94.9	215	7 ADF11419	Adf11419 22B3 anti
20	538	94.7	108	8 ADS19298	Ads19298 Light cha
21	536	94.4	108	9 ADM08866	Adw08866 IGF-IR an
22	535	94.2	108	8 ADI22138	Adi22138 Anti-plat
23	534	94.0	108	9 AEB01057	Aeb01057 Human IP1
24	534	94.0	109	7 ADF11403	Adf11403 2D8 anti-

25	534	94.0	109	7 ADF11415	Adf11415 9H7 anti-
26	534	94.0	215	7 ADF11439	Adf11439 9H7 anti-
27	534	94.0	215	7 ADF11427	Adf11427 2D8 anti-
28	531.5	93.6	129	6 ABP57362	Abp57362 Anti-TRAI
29	529.5	93.2	107	6 ABR54916	AbR54916 Light cha
30	529.5	93.2	107	9 AEB19292	Aeb19292 IGG kappa
31	529.5	93.2	236	9 AD251040	Adz51040 Amino aci
32	529	93.1	128	7 ADJ73528	Adj73528 Erythropro
33	529	93.1	251	5 ABP45038	Abp45038 Human BLY
34	529	93.1	251	7 ADG95865	Adg95865 Single ch
35	528.5	93.0	129	7 ADJ73532	Adj73532 Erythropro
36	525	92.4	109	4 AAB62756	Aab62756 Human HIV
37	524.5	92.3	107	9 ADY26776	Ady26776 Anti-NGF-
38	524.5	92.3	110	9 ADX02205	Adx02205 SARS coro
39	524.5	92.3	110	9 ADX02049	Adx02049 SARS coro
40	524.5	92.3	214	8 ADH34591	Adh34591 023 light
41	524.5	92.3	251	9 ADX01956	Adx01956 SARS coro
42	524.5	92.3	252	9 ADX02034	Adx02034 SARS coro
43	524	92.3	108	9 ADM08864	Adw08864 IGF-IR an
44	524	92.3	108	9 AEB01064	Aeb01064 Human IP1
45	523.5	92.2	224	4 AAB99371	Aab99371 Human int

ALIGNMENTS

RESULT 1  
AAM51165  
ID AAM51165 standard; protein; 108 AA.  
XX

AC AAM51165;

XX 10-JUN-2002 (first entry)

XX Anti-tumour necrosis factor antibody light chain variable region.

KW Tumour necrosis factor alpha; TNF; antibody; light chain; CDR;  
KW complementarity determining region; antirheumatic; antiarthritic;  
KW antiulcer; antiasthmatic; antiallergic; antiinflammatory; antisickling;  
KW antidiabetic; antiarteriosclerotic; antiatherosclerotic; vasotropic;  
KW antiangular; cardiant; antibacterial; virucide; fungicide; antileprotic;  
KW protozoacide; cytostatic; neuroprotective; antiparkinsonian; nootropic;  
XX human; diagnosis; therapy.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Region 1. .23

FT /label= FR1

FT Region 24. .34

FT /label= CDR1

FT Region 35. .49

FT /label= FR2

FT Region 50. .56

FT /label= CDR2

FT Region 57. .88

FT /label= FR3

FT Region 89. .98

FT /label= CDR3

FT Region 99. .108

FT /label= J6

XX WO200212502-A2.

PN 14-FEB-2002.

XX 07-AUG-2001; 2001WO-US024785.

PR 07-AUG-2000; 2000US-0223360P.

PR 29-SEP-2000; 2000US-0236826P.

PR 01-AUG-2001; 2001US-00920137.

XX (CENZ ) CENTOCOR INC.

PA



XX  
PI Giles-Komar J, Knight DM, Heavner G, Scallion B, Shealy D;  
XX WPI; 2002-217194/27.  
XX  
XX Novel isolated mammalian anti-tumor necrosis factor antibody, useful for  
PT treating sickle cell anemia, diabetes, atherosclerosis, restenosis,  
PT angina pectoris, myocardial infarction, leprosy.  
XX  
XX Claim 9; Page 129-130; 131pp; English.  
XX  
XX The present sequence is that of the light chain variable region of an  
CC anti-tumour necrosis factor (TNF) antibody of the invention. The  
CC invention provides isolated human, primate, rodent, mammalian, chimeric,  
CC humanised and/or complementarity determining region (CDR)-grafted anti-  
CC TNF antibodies, immunoglobulins, cleavage products and other specified  
CC portions and variants, as well as anti-TNF antibody compositions,  
CC encoding or complementary nucleic acids, vectors, host cells,  
CC compositions, formulations, devices, transgenic animals, transgenic  
CC plants, and methods of making and using them. The anti-TNF antibody  
CC comprises at least a portion of an immunoglobulin molecule, especially  
CC the heavy chain and/or light chain variable regions given in AAM51164 and  
CC in the present sequence, or either all of the CDRs of the heavy chain  
CC (see AAM51158-60) or all of the CDRs of the light chain (see AAM51161-  
CC 63). The antibody may inhibit TNF-induced cell adhesion molecules,  
CC inhibit TNF binding to receptor, or provide Arthritic Index improvement  
CC in a mouse model. It is useful for diagnosing or treating a TNF related  
CC arthritis, gastric ulcer, asthma, allergic rhinitis, Crohn's pathology,  
CC sickle cell anaemia, diabetes, a cardiovascular disease such as  
CC arteriosclerosis, atherosclerosis, restenosis, angina pectoris or  
CC myocardial infarction, an infectious disease in a cell such as bacterial,  
CC viral, and fungal infections, pneumonia, leprosy and malaria, a malignant  
CC disease such as leukaemia, chronic myelocytic leukaemia, Burkitt's  
CC lymphoma and multiple myeloma, or a neurological disease such as multiple  
CC sclerosis, Parkinson's disease, spinal ataxia, Alzheimer's disease and  
CC Creutzfeldt-Jakob disease  
XX  
SQ Sequence 108 AA;  
  
Query Match 98.4%; Score 559; DB 5; Length 108;  
Best Local Similarity 99.1%; Pred. No. 1.le-37;  
Matches 107; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQQKPGQAPRLLIYDASNRTGIPA 60  
|||  
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQQKPGQAPRLLIYDASNRTGIPA 60  
  
QY 61 RFGSGSGTDFTLTISLSEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108  
|||  
Db 61 RFGSGSGTDFTLTISLSEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108  
  
RESULT 2  
AAM51173  
ID AAM51173 standard; protein; 108 AA.  
XX  
AC AAM51173;  
XX  
DT 10-JUN-2002 (first entry)  
XX  
DE Human Vg/38K-type light chain variable region.  
XX  
KW Tumour necrosis factor alpha; TNF; antibody; light chain; CDR;  
KW complementarity determining region; antirheumatic; antiarthritic;  
KW antiulcer; antiasthmatic; antiallergic; antiinflammatory; antisickling;  
KW antidiabetic; antiarteriosclerotic; antiatherosclerotic; vasotropic;  
KW antiangular; cardiant; antibacterial; virucide; fungicide; antileprotic;  
KW protozoacide; cytostatic; neuroprotective; antiparkinsonian; nootropic;  
KW human; diagnosis; therapy; Vg/38K.  
XX  
OS Homo sapiens.  
XX

FH Key Location/Qualifiers  
FT Region 1. .23  
FT /label= FR1  
FT Region 24. .34  
FT /label= CDR1  
FT Region 35. .49  
FT /label= FR2  
FT Region 50. .56  
FT /label= CDR2  
FT Region 57. .88  
FT /label= FR3  
FT Region 89. .98  
FT /label= CDR3  
FT Region 99. .108  
FT /label= J3  
  
WO200212502-A2.  
  
14-FEB-2002.  
  
07-AUG-2001; 2001WO-US024785.  
  
07-AUG-2000; 2000US-0223360P.  
29-SEP-2000; 2000US-0236826P.  
01-AUG-2001; 2001US-00920137.  
  
(CENZ ) CENTOCOR INC.  
  
Giles-Komar J, Knight DM, Heavner G, Scallion B, Shealy D;  
  
WPI; 2002-217194/27.  
N-PSDB; ABL53513.  
  
Novel isolated mammalian anti-tumor necrosis factor antibody, useful for  
treating sickle cell anemia, diabetes, atherosclerosis, restenosis,  
angina pectoris, myocardial infarction, leprosy.  
  
Example 3; Fig 5; 131pp; English.  
  
The present sequence is that of a human Vg/38K-type light chain variable  
region encoded by a human germline gene in a transgenic mouse used in  
human monoclonal antibody (mAb) construction. A GentNV fusion was  
performed using spleen cells from a hybrid mouse containing human  
variable and constant region antibody transgenes that was immunised with  
recombinant human tumour necrosis factor (TNF) alpha. Human mAbs were  
obtained that bound immobilised human TNF alpha with apparently high  
avidity. These mAbs had a totally human IgG1, kappa isotype. The mature  
portion of the light chain variable region of 2 of the mAbs, TNV14 and  
TNV15, were identical (see AAM51174) to the present sequence, while the  
light chain variable region of 2 others, TNV148(B) and TNV196 (see  
AAM51175), differed by a single amino acid residue. The invention  
provides human, primate, rodent, mammalian, chimeric, humanised and/or  
complementarity determining region (CDR)-grafted anti-TNF antibodies,  
antibody compositions, and cleavage products and variants, as well as anti-TNF  
host cells, compositions, formulations, devices, transgenic animals,  
transgenic plants, and methods of making and using them. The anti-TNF  
antibody comprises at least a portion of an immunoglobulin molecule,  
especially the heavy chain and/or light chain variable regions given in  
the present sequence and in AAM51165, or either all of the CDRs of the  
heavy chain (see AAM51158-60) or all of the CDRs of the light chain (see  
AAM51161-63). The antibodies may inhibit TNF-induced cell adhesion  
molecules, inhibit TNF binding to receptor, or provide Arthritic Index  
improvement in a mouse model. They are useful for diagnosing or treating  
a TNF related condition in a cell, tissue, organ or animal (claimed) such  
as rheumatoid arthritis, gastric ulcer, asthma, allergic rhinitis,  
Crohn's pathology, sickle cell anaemia, diabetes, a cardiovascular  
disease such as arteriosclerosis, atherosclerosis, restenosis, angina  
pectoris or myocardial infarction, an infectious disease in a cell such  
as bacterial, viral, and fungal infections, pneumonia, leprosy and  
malaria, a malignant disease such as leukaemia, chronic myelocytic  
leukaemia, Burkitt's lymphoma and multiple myeloma, or a neurological  
disease such as multiple sclerosis, Parkinson's disease, spinal ataxia,

CC Alzheimer's disease and Creutzfeldt-Jakob disease  
XX Sequence 108 AA;  
SQ Query Match 98.4%; Score 559; DB 5; Length 108;  
Best Local Similarity 99.1%; Pred. No. 1.1e-37;  
Matches 107; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQQKPGQAPRLLIYDASNRTGIPA 60  
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQQKPGQAPRLLIYDASNRTGIPA 60  
  
QY 61 RFSGSGSGTDFTLTITSSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108  
Db 61 RFSGSGSGTDFTLTITSSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108  
  
RESULT 3  
AAU76334  
ID AAU76334 standard; peptide; 108 AA.  
XX  
AC AAU76334;  
XX  
DT 21-MAY-2002 (first entry)  
XX  
DE Human anti-dual integrin antibody complete variable region #2.  
XX  
KW Human; antibody; dual integrin; HC CDR; variable region; LC CDR;  
KW medical device; immune related disease; rheumatoid arthritis;  
KW gastric ulcer; asthma; allergic rhinitis; Crohn's pathology;  
KW sickle cell anaemia; diabetes; cardiovascular disease; arteriosclerosis;  
KW atherosclerosis; restenosis; angina pectoris; myocardial infarction;  
KW infectious disease; pneumonia; leprosy; malaria; malignant disease;  
KW leukaemia; chronic myelocytic leukaemia; multiple myeloma;  
KW neurological disease; multiple sclerosis; Parkinson's disease;  
KW Alzheimer's disease; Creutzfeldt-Jakob disease.  
XX  
OS Homo sapiens.  
XX  
PN WO200212501-A2.  
XX  
PD 14-FEB-2002.  
XX  
PF 07-AUG-2001; 2001WO-US024784.  
XX  
PR 07-AUG-2000; 2000US-0223363P.  
PR 01-AUG-2001; 2001US-00920267.  
XX  
PA (CENZ ) CENTOCOR INC.  
XX  
PI Giles-Komar J, Heavner G, Snyder L, Trikha M;  
XX WPI; 2002-217193/27.  
XX  
PT Novel isolated mammalian anti-dual integrin antibody, useful for  
PT diagnosing or treating dual integrin related condition such as rheumatoid  
PT arthritis, gastric ulcer, asthma, atherosclerosis, restenosis.  
XX  
PS Claim 1; Page 134; 144pp; English.  
XX  
CC The invention relates to an isolated mammalian anti-dual integrin  
CC antibody having at least one of the human heavy chain or light chain  
CC complementary determining region (CDR, HC CDR1-CDR3, LC CDR1-3). Also  
CC included are the nucleic acids encoding the CDRs, a vector comprising the  
CC nucleic acids, a host cell comprising the vector, an anti-idiotypic  
CC antibody that binds to the ant-dual integrin, a medical device comprising  
CC the antibody suitable for administration by parenteral, subcutaneous,  
CC intramuscular, intravenous, intrarticular, intrabronchial,  
CC intraabdominal, intracapsular, intracartilaginous, intracavitary,  
CC intracerebellar, or other routes as given in specification. The antibody  
CC is useful for diagnosing or treating a dual integrin related condition in  
CC an animal for example, immune related disease such as rheumatoid  
CC arthritis, gastric ulcer, asthma, allergic rhinitis, Crohn's pathology,

CC sickle cell anaemia, diabetes, cardiovascular disease such as  
CC arteriosclerosis, atherosclerosis, restenosis, angina pectoris,  
CC myocardial infarction, infectious disease in a cell such as bacterial,  
CC viral, and fungal infections, pneumonia, leprosy, malaria; malignant  
CC disease such as leukaemia, chronic myelocytic leukaemia, Burkitt's  
CC lymphoma, multiple myeloma; neurological disease such as multiple  
CC sclerosis, Parkinson's disease, spinal ataxia, Alzheimer's disease,  
CC Creutzfeldt-Jakob disease and many other diseases given in the  
CC specification. The present sequence is an anti-dual integrin human  
CC variable region containing at least one of the six CDRs listed above  
CC (AAU76327-AAU76332)  
XX  
SQ Sequence 108 AA;  
  
Query Match 98.4%; Score 559; DB 5; Length 108;  
Best Local Similarity 99.1%; Pred. No. 1.1e-37;  
Matches 107; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQQKPGQAPRLLIYDASNRTGIPA 60  
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQQKPGQAPRLLIYDASNRTGIPA 60  
  
QY 61 RFSGSGSGTDFTLTITSSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108  
Db 61 RFSGSGSGTDFTLTITSSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108  
  
RESULT 4  
ADJ73533  
ID ADJ73533 standard; protein; 108 AA.  
XX  
AC ADJ73533;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE Erythropoietin light chain mimetibody SeqID 989.  
XX  
KW mimetic; CDR mimetibody; gene therapy; transgenic; immune;  
KW cardiovascular; infectious; malignant; neurologic disease; anaemia;  
KW immunomodulator; cardiant; antimicrobial; cytostatic; neuroprotective;  
KW erythropoietin.  
XX  
OS Synthetic.  
XX  
PN WO2003084477-A2.  
XX  
PD 16-OCT-2003.  
XX  
PF 24-MAR-2003; 2003WO-US009139.  
XX  
PR 29-MAR-2002; 2002US-0368791P.  
XX  
PA (CENZ ) CENTOCOR INC.  
XX  
PI Heavner GA, Knight DM, Scallion BJ, Ghrayeb J;  
XX WPI; 2003-804237/75.  
XX  
PT New CDR mimetibody comprising a portion of a heavy or light chain  
PT variable region comprising human framework or ligand binding region,  
PT useful for preparing a composition for treating e.g., immune,  
PT cardiovascular or neurologic disease.  
XX  
PS Example 2; SEQ ID NO 989; 97pp; English.  
XX  
CC This invention relates to novel mammalian CDR mimetibodies, specific  
CC portions or variants thereof. Specifically, it refers to an antibody  
CC fragment where a protein has been inserted into, or replaces a portion  
CC of, one or more CDR regions, such that each CDR mimetibody comprises at  
CC least one portion of a heavy chain or light chain variable region, which  
CC itself comprises at least one human framework region and at least one  
CC ligand binding region (LBR). The present invention describes human  
CC mimetibodies, including modified immunoglobulins and cleavage products







KW antiulcer; antiasthmatic; antiallergic; antiinflammatory; antisickling;  
KW antidiabetic; antiarteriosclerotic; antiatherosclerotic; vasotropic;  
KW antiangular; cardiant; antibacterial; virucide; fungicide; antileprotic;  
KW protozoacide; cytostatic; neuroprotective; antiparkinsonian; nootropic;  
KW human; diagnosis; therapy; TNV148(B); TNV196; monoclonal antibody; mAb.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1. .20  
FT /label= Signal\_peptide  
FT Protein 20. .129  
FT /label= Mature\_protein  
FT Region 21. .43  
FT /label= FR1  
FT Region 44. .54  
FT /label= CDR1  
FT Region 55. .69  
FT /label= FR2  
FT Region 70. .76  
FT /label= CDR2  
FT Region 77. .108  
FT /label= FR3  
FT Region 109. .118  
FT /label= CDR3  
FT Region 119. .129  
FT /label= J3  
XX  
PN WO200212502-A2.  
XX  
PD 14-FEB-2002.  
XX  
PF 07-AUG-2001; 2001WO-US024785.  
XX  
PR 07-AUG-2000; 2000US-0223360P.  
PR 29-SEP-2000; 2000US-0236826P.  
PR 01-AUG-2001; 2001US-00920137.  
XX  
PA (CENZ ) CENTOCOR INC.  
XX  
PI Giles-Komar J, Knight DM, Heavner G, Scallon B, Shealy D;  
XX  
DR WPI; 2002-217194/27.  
DR N-PSDB; ABL53515.  
XX  
PT Novel isolated mammalian anti-tumor necrosis factor antibody, useful for  
PT treating sickle cell anemia, diabetes, atherosclerosis, restenosis,  
PT angina pectoris, myocardial infarction, leprosy.  
XX  
PS Example 3; Fig 5; 131pp; English.  
XX  
CC The present sequence is that of the light chain variable region of anti-  
CC tumour necrosis factor (TNF) human recombinant monoclonal antibodies  
CC (mAbs) TNV148(B) and TNV196. These are human mAbs produced from a GentNV  
CC fusion using spleen cells from a hybrid mouse containing human variable  
CC and constant region antibody transgenes that was immunised with human TNF  
CC alpha. The human mAbs bind immobilised human TNF alpha with high avidity  
CC and have a totally human IgG1, kappa isotype. The mature portion of the  
CC light chain variable region differs from that of the Vg/38-type light  
CC chain germline sequence (see AAM51173) by a single residue (Tyr-50  
CC replacing Ser). The light chain variable regions of 2 other human mAbs  
CC (see AAM51174) were identical to the germline sequence. The invention  
CC provides isolated human, primate, rodent, mammalian, chimeric, humanised  
CC and/or complementarity determining region (CDR)-grafted anti-TNF  
CC antibodies, immunoglobulins, cleavage products and other specified  
CC portions and variants, as well as anti-TNF antibody compositions,  
CC encoding or complementary nucleic acids, vectors, host cells,  
CC compositions, formulations, devices, transgenic animals, transgenic  
CC plants, and methods of making and using them. The anti-TNF antibody  
CC comprises at least a portion of an immunoglobulin molecule, especially  
CC the heavy chain and/or light chain variable regions given in the present  
CC sequence and in AAM51165, or either all of the CDRs of the heavy chain  
CC (see AAM51158-60) or all of the CDRs of the light chain (see AAM51161-

CC 63). The antibodies may inhibit TNF-induced cell adhesion molecules,  
CC inhibit TNF binding to receptor, or provide Arthritic Index improvement  
CC in a mouse model. They are useful for diagnosing or treating a TNF  
CC related condition in a cell, tissue, organ or animal (claimed) such as  
CC rheumatoid arthritis, gastric ulcer, asthma, allergic rhinitis, Crohn's  
CC pathology, sickle cell anaemia, diabetes, a cardiovascular disease such  
CC as arteriosclerosis, atherosclerosis, restenosis, angina pectoris or  
CC myocardial infarction, an infectious disease in a cell such as bacterial,  
CC viral, and fungal infections, pneumonia, leprosy and malaria, a malignant  
CC disease such as leukaemia, chronic myelocytic leukaemia, Burkitt's  
CC lymphoma and multiple myeloma, or a neurological disease such as multiple  
CC sclerosis, Parkinson's disease, spinal ataxia, Alzheimer's disease and  
CC Creutzfeldt-Jakob disease  
XX  
SQ Sequence 129 AA;  
  
Query Match 98.4%; Score 559; DB 5; Length 129;  
Best Local Similarity 99.1%; Pred. No. 1.3e-37;  
Matches 107; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60  
Db |||||  
QY 21 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 80  
Db |||||  
QY 61 RFGSGSGTDFLTLTISLSEPEDFAVVYCCQQRSNWPPFTFGPTKVDIK 108  
Db |||||  
QY 81 RFGSGSGTDFLTLTISLSEPEDFAVVYCCQQRSNWPPFTFGPTKVDIK 128  
  
RESULT 9  
AAB72884  
ID AAB72884 standard; protein; 108 AA.  
XX  
AC AAB72884;  
XX  
DT 10-MAY-2001 (first entry)  
XX  
DE Human anti-HER2/neu antibody 2-E8 light chain.  
XX  
KW Human; HER2; neu; erbB2; oncogene; cancer; antibody; immunotherapy; 3-F2;  
KW 1-D2; 2-E8; growth factor receptor.  
XX  
OS Homo sapiens.  
XX  
PN WO200109187-A2.  
XX  
PD 08-FEB-2001.  
XX  
PF 25-JUL-2000; 2000WO-US020272.  
XX  
PR 29-JUL-1999; 99US-0146313P.  
PR 10-MAR-2000; 2000US-0188539P.  
XX  
PA (MEDA-) MEDAREX INC.  
XX  
PI Keler T, Deo Y;  
XX  
DR WPI; 2001-168698/17.  
DR N-PSDB; AAF75590.  
XX  
PT New human monoclonal antibody that specifically binds to growth factor  
PT receptor HER2/neu, for treating, preventing or diagnosing diseases  
PT characterized by aberrant HER2/neu expression e.g. cancers.  
XX  
PS Disclosure; Page 110; 113pp; English.  
XX  
CC The present invention provides the protein and coding sequences for human  
CC monoclonal antibodies which bind specifically to the HER2/neu growth  
CC factor receptor (also known as erbB2). These are designated 3-F2, 1-D2  
CC and 2-E8. They can be used in the immunotherapy-based treatment and  
CC prognosis of cancers, particularly adenocarcinomas such as salivary  
CC gland, stomach, kidney, mammary gland, lung and squamous cell carcinomas,  
CC and ovarian cancer. The present sequence is part of an antibody of the



CC invention  
XX Sequence 108 AA;  
SQ  
Query Match 95.2%; Score 541; DB 4; Length 108;  
Best Local Similarity 95.4%; Pred. No. 3e-36;  
Matches 103; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
QY 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQKPGQAPRLLIYDASNRATGIPA 60  
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQKPGQAPRLLIYDASNRATGIPA 60  
QY 61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPTKVDIK 108  
Db 61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPYTFGQGTKLEIK 108  
RESULT 10  
AEB01062  
ID AEB01062 standard; protein; 108 AA.  
XX AEB01062;  
AC  
XX  
DT 08-SEP-2005 (first entry)  
XX Human IP10 antibody light chain variable region, SEQ ID NO 90.  
DE  
XX antibody; IP-10; inflammation; immune disorder; dermatological disease;  
KW respiratory disease; neurological disease; degeneration; infection;  
KW Neuroprotective; Antiarthritic; Antirheumatic; Antiinflammatory;  
KW Gastrointestinal-Gen.; Anticancer; Dermatological; Immunosuppressive;  
KW Antidiabetic; Antipsoriatic; Antithyroid; Antiasthmatic;  
KW Respiratory-Gen.; Cerebroprotective; Vasotropic; Nootropic;  
KW Antiparkinsonian; Antiangiogenic; Antiartherosclerotic; Virucide;  
KW Antibacterial; light chain variable region.  
XX  
OS Homo sapiens.  
XX WO2005058815-A2.  
PN  
XX  
XX 30-JUN-2005.  
XX  
PF 10-DEC-2004; 2004WO-US041506.  
XX  
XX 10-DEC-2003; 2003US-0529180P.  
PR  
XX (MEDA-) MEDAREX INC.  
PA  
XX Deshpande S, Huang H, Srinivasan M, Cardarelli JM, Wang C;  
PI Passmore D, Rangan VS, Lane TB, Keirstead HS, Liu MT;  
PI  
XX WPI; 2005-467095/47.  
DR N-PSDB; AEB01088.  
XX  
XX Isolated human monoclonal antibody or an antigen-binding portion, which  
PT specifically binds to human interferon gamma inducible protein 10 (IP-  
PT 10), useful for treating viral or bacterial infection, or inflammatory or  
PT autoimmune diseases.  
XX  
PS Claim 35; SEQ ID NO 90; 179pp; English.  
XX  
CC The invention relates to an isolated human monoclonal antibody or an  
CC antigen-binding portion, which specifically binds to human IP-10 and  
CC exhibits at least one property selected from: inhibits binding of IP-10  
CC to CXCR3; inhibits IP-10 induced calcium flux; inhibits IP-10 induced  
CC cell migration; cross-reacts with rhesus monkey IP-10; does not cross-  
CC react with mouse IP-10; does not cross-react with human MIG; or does not  
CC cross-react with human ITAC. The isolated human monoclonal antibody is  
CC useful for treating an inflammatory or autoimmune disease including  
CC multiple sclerosis, rheumatoid arthritis, inflammatory bowel disease  
CC (e.g., ulcerative colitis, Crohn's disease), systemic lupus  
CC erythematosus, Type I diabetes, inflammatory skin disorders (e.g.,  
CC psoriasis, lichen planus), autoimmune thyroid disease (e.g., Graves'

CC disease, Hashimoto's thyroiditis), Sjogren's syndrome, pulmonary  
CC inflammation (e.g., asthma, chronic obstructive pulmonary disease,  
CC pulmonary sarcoidosis, lymphocytic alveolitis), transplant rejection,  
CC spinal cord injury, brain injury (e.g., stroke), neurodegenerative  
CC diseases (e.g., Alzheimer's disease, Parkinson's disease), gingivitis,  
CC gene therapy-induced inflammation, diseases of angiogenesis, inflammatory  
CC kidney disease (e.g., IgA nephropathy, membranoproliferative  
CC glomerulonephritis, rapidly progressive glomerulonephritis), or  
CC atherosclerosis. It is also useful for treating a viral or bacterial  
CC infection involving unwanted IP-10 activity in a subject, where the viral  
CC infection is mediated by HIV, HCV, HSV-1 or SARS virus. The present  
CC sequence represents the amino acid sequence of a human IP10 monoclonal  
CC antibody light chain variable region.  
XX  
SQ Sequence 108 AA;  
Query Match 95.2%; Score 541; DB 9; Length 108;  
Best Local Similarity 95.4%; Pred. No. 3e-36;  
Matches 103; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
QY 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQKPGQAPRLLIYDASNRATGIPA 60  
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQKPGQAPRLLIYDASNRATGIPA 60  
QY 61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPTKVDIK 108  
Db 61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPYTFGQGTKLEIK 108  
RESULT 11  
ADF11411  
ID ADF11411 standard; protein; 109 AA.  
XX ADF11411;  
AC  
XX 12-FEB-2004 (first entry)  
DT  
XX 16E1 anti-OPGL antibody kappa chain variable region SEQ ID NO:24.  
DE  
XX human; antibody; osteoprotegerin ligand; OPGL; osteopenic disorder;  
KW osteopathic; antiarthritic; cytostatic; gene therapy; bone disorder;  
KW osteoporosis; bone loss; arthritis; Paget's disease; osteopenia.  
XX  
OS Homo sapiens.  
XX WO2003086289-A2.  
PN  
XX 23-OCT-2003.  
PD  
XX 07-APR-2003; 2003WO-US010749.  
PF  
XX 05-APR-2002; 2002US-0370407P.  
PR  
XX (AMGE-) AMGEN INC.  
PA  
XX Boyle WJ, Medlock E, Sullivan JK, Elliott RL, Martin F, Huang H;  
PI WPI; 2003-845253/78.  
XX N-PSDB; ADF11410.  
DR  
XX New isolated antibody that specifically binds osteoprotegerin ligand,  
PT useful for diagnosing or treating bone disorders, such as osteoporosis,  
PT bone loss from arthritis, Paget's disease or osteopenia.  
XX  
PS Claim 6; SEQ ID NO 24; 156pp; English.  
XX  
CC The present invention describes an isolated human antibody (I) that  
CC specifically binds osteoprotegerin ligand (OPGL). Also described: (1) a  
CC pharmaceutical composition comprising a pharmaceutical carrier and a  
CC therapeutic amount of (I); (2) methods of treating an osteopenic disorder  
CC in a patient, comprising administering to a patient the pharmaceutical  
CC composition of (1) or a pharmaceutical amount of (I); and (3) a method  
CC for detecting OPGL in a biological sample, comprising contacting the

sample with (I) under conditions that allow for binding of the antibody to OPGL, and measuring the level of bound antibody in the sample. (I) has osteopathic, antiarthritic and cytostatic activities, and can be used in gene therapy. The composition and methods are useful in diagnosing or treating bone disorders, such as osteoporosis, bone loss from arthritis, Paget's disease or osteopenia. The antibody (I) may also be used for detecting OPGL in biological samples and in identifying cells or tissues that produce the protein. The present sequence represents a sequence which is used in the exemplification of the present invention.

Sequence 109 AA;

```

Query Match          95.2%; Score 541; DB 7; Length 109;
Best Local Similarity 95.4%; Pred. No. 3.1e-36;
Matches 103; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

```

<b>Qy</b>	1 EIVLTQSPATLSLSPGERATLSCRASQSISVSYLAWYQQKPGAPRLIIYDASNRATGIPA 60
<b>D<sub>b</sub></b>	1 EIVLTQSPATLSLSPGERATLSCRASQSISVSYLAWYQQKPGAPRLIIYDASNRATGIPA 60

RESULT 12  
ADFF11435  
ID ADF11435 standard; protein; 215 AA.  
XX  
AC ADF11435;  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE 16E1 anti-OPGL antibody light chain SEQ ID NO:48.  
XX  
KW human; antibody; osteoprotegerin ligand; OPGL; osteopenic disorder;  
KW osteopathic; antiarthritic; cytostatic; gene therapy; bone disorder;  
KW osteoporosis; bone loss; arthritis; Paget's disease; osteopenia.  
KW osteoporosis; bone loss; arthritis; Paget's disease; osteopenia.

The present invention describes an isolated human antibody (I) that specifically binds osteoprotegerin ligand (OPGL). Also described: (1) a pharmaceutical composition comprising a pharmaceutical carrier and a therapeutic amount of (I); (2) methods of treating an osteopenic disorder in a patient, comprising administering to a patient the pharmaceutical composition of (1) or a pharmaceutical amount of (I); and (3) a method for detecting OPGL in a biological sample, comprising contacting the sample with (I) under conditions that allow for binding of the antibody to OPGL, and measuring the level of bound antibody in the sample. (I) has osteopathic, antiarthritic and cytostatic activities, and can be used in gene therapy. The composition and methods are useful in diagnosing or

treating bone disorders, such as osteoporosis, bone loss from arthritis, Paget's disease or osteopenia. The antibody (I) may also be used for detecting OPGL in biological samples and in identifying cells or tissues that produce the protein. The present sequence represents a sequence which is used in the exemplification of the present invention.

Sequence 215 AA;

```
Query Match          95.2%; Score 541; DB 7; Length 215;
Best Local Similarity 95.4%; Pred. No. 5.8e-36;
Matches 103; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
```

Qy	1	EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQQKPGQAPRLIIVDASNRATGIPA	60
db	1	EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQQKPGQAPRLIIVDASNRATGIPA	60

RESULT 13  
ADM41547  
ID ADM41547 standard; protein; 128 AA.  
XX  
XX  
XX ADM41547;  
DT 03-JUN-2004 (first entry)

The present sequence is that of human anti-interleukin-1 receptor type 1 (IL-1R1) monoclonal antibody (Mab) 26F5 kappa chain variable region. Human MAb's to IL-1R1 were prepared using the HCo7 strain of transgenic mice, which expresses human antibody genes. These mice were immunised with purified recombinant IL-1R1, and splenocytes from immunised mice were fused to a mouse myeloma cell line to generate hybridomas. Hybridomas which secreted a MAb that bound with high avidity to IL-1R1 were selected. The MABs inhibit IL-1 signalling by competing with IL-1beta and IL-1alpha binding to IL-1R. These MABs, as well as single chain antibodies single chain Fv antibodies, Fab antibodies, Fab' antibodies and (Fab')2 antibodies derived from them, are used in methods of treating

CC IL-1 mediated diseases or for detecting the amount of IL-1R1 in a sample.  
CC IL-1 mediated diseases include acute pancreatitis, amyotrophic lateral  
CC sclerosis, Alzheimer's disease, cachexia, anorexia, asthma,  
CC atherosclerosis, autoimmune vasculitis, chronic fatigue syndrome,  
CC Clostridium associated illnesses, coronary conditions, cancer including  
CC leukaemia and tumour metastasis, diabetes, endometriosis, fever,  
CC fibromyalgia, glomerulonephritis, graft versus host disease,  
CC osteoarthritis, rheumatoid arthritis, inflammatory eye disease,  
CC ischaemia, Kawasaki's disease, learning impairment, lung diseases,  
CC multiple sclerosis, myopathy, osteoporosis, pain, Parkinson's disease,  
CC periodontal disease, pre-term labour, psoriasis, reperfusion injury,  
CC septic shock, side effects of radiation therapy, temporal mandibular  
CC joint disease, sleep disturbance, uveitis, or an inflammatory condition  
CC resulting from strain, sprain, cartilage damage, trauma, orthopaedic  
CC surgery, infection or other disease processes.

XX SQ Sequence 128 AA;

Query Match 95.1%; Score 540; DB 8; Length 128;  
Best Local Similarity 96.3%; Pred. No. 4.3e-36;  
Matches 104; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQQKPGQAPRLLIYDASNRTGIPA 60  
Db 21 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQQKPGQAPRLLIYDASNRTGIPA 80  
Qy 61 RFSGSGSGTDFTLTISLSEPEDEFAVYYCQQRSNWPPFTFGGTKVDIK 108  
Db 81 RFSGSGSGTDFTLTISLSEPEDEFAVYYCQQRSNWPPPLTFGGGTVKVEIK 128

RESULT 14

ADD89877  
ID ADD89877 standard; protein; 130 AA.  
XX  
AC ADD89877;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Human anti-TNF antibody 9E7 light chain variable region.  
XX  
KW Human; Tumour necrosis factor; TNF; antibody; cytostatic; anabolic;  
KW eating-disorders-gen; immunomodulator; antimicrobial; cardiovascular-gen;  
KW neuroprotective.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Region 44. .54  
FT /note= "CDR1"  
FT Region 65. .71  
FT /note= "CDR2"  
FT Region 109. .118  
FT /note= "CDR3"  
XX  
PN WO2003083061-A2.  
XX  
PD 09-OCT-2003.  
XX  
PF 24-MAR-2003; 2003WO-US009072.  
XX  
PR 26-MAR-2002; 2002US-0367903P.  
XX  
PA (CENZ ) CENTOCOR INC.  
XX  
PI Giles-Komar J, Scallion BJ, Carton JM;  
XX  
DR WPI; 2003-804040/75.  
DR N-PSDB; ADD89883.  
XX  
PT New isolated mammalian anti-tumor necrosis factor (TNF) antibody, useful  
PT for diagnosing or treating an anti-TNF related condition, e.g. cancer,  
PT anorexia, cachexia, or bacterial infection.

XX Claim 1; Fig 3B; 87pp; English.  
PS  
XX  
CC The present sequence is that of the light chain variable region of human  
CC anti-tumour necrosis factor (TNF) monoclonal antibody 9E7. This human TNF  
CC reactive IgG monoclonal antibody was generated by cloning variable and  
CC constant region DNA in vector pC4 and expression in CHO cells. The  
CC invention provides isolated human, primate, rodent, mammalian, chimeric,  
CC humanized and/or CDR-grafted anti-TNF antibodies, immunoglobulins, their  
CC cleavage products, other specified portions and variants, as well as anti  
CC -TNF antibody compositions, nucleic acids encoding these, vectors, host  
CC cells, methods for producing the antibodies using a host cell, transgenic  
CC animal or transgenic plant or plant cell, and therapeutic compositions,  
CC methods and devices. The antibody, nucleic acid, protein, composition and  
CC methods are useful for diagnosing or treating an anti-TNF related  
CC condition, e.g. cancer, anorexia, cachexia, or an immune, cardiovascular,  
CC infectious, and/or neurological disease.

XX SQ Sequence 130 AA;

Query Match 95.1%; Score 540; DB 7; Length 130;  
Best Local Similarity 96.3%; Pred. No. 4.3e-36;  
Matches 104; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQQKPGQAPRLLIYDASNRTGIPA 60  
Db 21 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQQKPGQAPRLLIYDASNRTGIPA 80  
Qy 61 RFSGSGSGTDFTLTISLSEPEDEFAVYYCQQRSNWPPFTFGGTKVDIK 108  
Db 81 RFSGSGSGTDFTLTISLSEPEDEFAVYYCQQRSNWPPPLTFGGGTVKVEIK 128

RESULT 15

ADS64664  
ID ADS64664 standard; protein; 130 AA.  
XX  
AC ADS64664;  
XX  
DT 16-DEC-2004 (first entry)  
XX  
DE Human 9E7LC light chain protein.  
XX  
KW Tumour necrosis factor; TNF; immunotherapy; TNF related diseases;  
KW obesity; immune related disease; rheumatoid arthritis;  
KW cardiovascular disease; stroke; malignant disease; leukaemia;  
KW neurological disease; multiple sclerosis; infection; hepatitis;  
KW anorectic; antiarthritic; cerebroprotective; vasotropic; cytostatic;  
KW neuroprotective; antibacterial; antiinflammatory; hepatotropic; virucide;  
KW human; 9E7LC; light chain.  
XX  
OS Homo sapiens.  
XX  
PN US2004185047-A1.  
XX  
PD 23-SEP-2004.  
XX  
PF 21-MAR-2003; 2003US-00394471.  
XX  
PR 21-MAR-2003; 2003US-00394471.  
XX  
PA (GILE/) GILES-KOMAR J.  
PA (SCAL/) SCALLON B J.  
PA (CART/) CARTON J M.  
XX  
PI Giles-Komar J, Scallion BJ, Carton JM;  
XX  
DR WPI; 2004-676151/66.  
DR N-PSDB; ADS64661.  
XX  
PT Novel isolated mammalian anti-tumor necrosis factor (TNF) alpha antibody  
PT capable of inhibiting binding of TNF alpha to TNF receptor, useful for  
PT treating TNF-related diseases such as obesity or rheumatoid arthritis.

```
XX
PS      Example 4; Fig 3; 45pp; English.
XX
CC      The present invention relates to a mammalian anti-tumour necrosis factor
CC      (TNF) antibody capable of inhibiting binding of TNF alpha to TNF
CC      receptor. The invention is useful for diagnosing or treating an anti-TNF
CC      related condition in a cell, tissue, organ or animal and in
CC      immunotherapy. The invention is also useful for treating TNF related
CC      diseases chosen from obesity, immune related disease such as rheumatoid
CC      arthritis, cardiovascular disease such as stroke, malignant disease such
CC      as leukaemia, neurological disease such as multiple sclerosis and
CC      bacterial or viral infections such as hepatitis. The present sequence is
CC      the human 9E7LC light chain protein (variable region and J-region). This
CC      sequence is used in the exemplification of the invention.
XX
SQ      Sequence 130 AA;

      Query Match          95.1%; Score 540; DB 8; Length 130;
      Best Local Similarity 96.3%; Pred. No. 4.3e-36;
      Matches 104; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1  EIVLTQSPATLSLSPGERATLSCRASQSVSYSLAWYQQKPGQAPRLLIYDASNRATGIPA 60
      |||||
Db      21 EIVLTQSPATLSLSPGERATLSCRASQSVSYSLAWYQQKPGQAPRLLIYDASNRATGIPA 80

QY      61 RFSGSGSGTDFTLTISLSEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
      |||||
Db      81 RFSGSGSGTDFTLTISLSEPEDFAVYYCQQRSNWPPFTFGGKVEIK 128

Search completed: December 28, 2005, 13:58:08
Job time : 128.462 secs
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OM protein - protein search, using sw model

Run on: December 28, 2005, 13:46:34 ; Search time 22.1538 Seconds  
(without alignments)  
469.057 Million cell updates/sec

Title: US-09-920-137F-8  
Perfect score: 568  
Sequence: 1 EIVLTQSPATLSLSPGERAT.....QQRSNWPPFTFGPGTKVDIK 108

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	528	93.0	114	2	S54905	Ig kappa chain V r
2	524.5	92.3	111	2	S23628	Ig kappa chain V r
3	519.5	91.5	144	2	PL0106	Ig kappa chain pre
4	517.5	91.1	128	2	A56701	Ig kappa chain V r
5	513.5	90.4	128	2	S40345	Ig kappa chain V-J
6	512.5	90.2	108	2	G44151	Ig kappa chain V r
7	510.5	89.9	129	2	S29627	Ig kappa chain V r
8	497.5	87.6	128	2	S40379	Ig kappa chain V-J
9	494.5	87.1	107	2	S57444	Ig kappa chain V-J
10	488.5	86.0	125	2	S40344	Ig kappa chain V-J
11	487	85.7	115	1	K3HUVG	Ig kappa chain pre
12	481	84.7	215	2	JE0244	Ig kappa chain NIG
13	473.5	83.4	106	2	PC4282	Ig kappa chain (an
14	472.5	83.2	114	2	S46375	Ig kappa chain V-J
15	471	82.9	115	2	S11697	Ig kappa chain pre
16	470.5	82.8	117	2	S40362	Ig kappa chain - h
17	467.5	82.3	107	2	S34005	Ig kappa chain V r
18	467.5	82.3	129	2	S40325	Ig kappa chain - h
19	464	81.7	129	2	S40363	Ig kappa chain - h
20	462.5	81.4	128	2	S40343	Ig kappa chain V-J
21	462	81.3	130	2	S40360	Ig kappa chain - h
22	460	81.0	109	2	A30608	Ig kappa chain V-I
23	459	80.8	116	2	B26555	Ig kappa chain V-I
24	459	80.8	131	2	S40328	Ig kappa chain - h
25	459	80.8	215	2	JE0242	Ig kappa chain NIG
26	458	80.6	109	2	H30601	Ig kappa chain V-I
27	458	80.6	109	2	S30601	Ig kappa chain V-I
28	458	80.6	109	2	PH0963	Ig kappa chain V r
29	456	80.3	92	2	S37506	Ig kappa chain V r

30	456	80.3	108	2	C30608	Ig kappa chain V-I
31	456	80.3	109	2	G30607	Ig kappa chain V-I
32	456	80.3	109	2	F30607	Ig kappa chain V-I
33	455.5	80.2	108	2	E30609	Ig kappa chain V-I
34	455	80.1	92	2	S37516	Ig kappa chain V r
35	455	80.1	109	2	C30601	Ig kappa chain V-I
36	455	80.1	109	2	D30601	Ig kappa chain V r
37	454	79.9	128	2	S20636	Ig kappa chain pre
38	454	79.9	129	1	K3HUHA	Ig kappa chain pre
39	453	79.8	109	1	K3HUPM	Ig kappa chain V-I
40	453	79.8	110	2	S20635	Ig kappa chain V r
41	453	79.8	129	1	K3HUHI	Ig kappa chain pre
42	452	79.6	109	2	G30601	Ig kappa chain V-I
43	452	79.6	129	2	S46369	IG light chain var
44	452	79.6	134	2	S38643	Ig kappa chain V r
45	448	78.9	108	2	B30608	Ig kappa chain V-I

ALIGNMENTS

RESULT 1  
S54905  
Ig kappa chain V region - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 08-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 21-Jan-2000  
C;Accession: S54905  
R;Esposito, G.; Traboni, C.  
submitted to the EMBL Data Library, November 1994  
A;Description: Cloning and sequencing of cDNA coding for the variable domains of a human  
A;Reference number: S54905  
A;Accession: S54905  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-114 <ESP>  
A;Cross-references: UNIPARC:UPI000011620A; EMBL:X82934; NID:g809554; PIDN:CAA58108.1; PI  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 93.0%; Score 528; DB 2; Length 114;  
Best Local Similarity 92.6%; Pred. No. 5e-39;  
Matches 100; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy	1	EIVLTQSPATLSLSPGERATLS	CRASQSVSYLA	WYQQKPGQAPRLLIYDASNRATGIPA	60
Db	1	DVVMTQSPATLSLSPGERATLS	CRASQSVSYLA	WYQQKPGQAPRLLIYDASRRATGIPA	60
Qy	61	RFGSGSGTDTLTITSSLEPED	FAVYQCQR	SNWPPFTFGPGTKVDIK	108
Db	61	RFGSGSGTDTLTITSSLEPED	FAVYQCQR	SNWPPLTFGGGTKVEIK	108

RESULT 2  
S23628  
Ig kappa chain V region - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 21-Jan-2000  
C;Accession: S23628  
R;Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deftos, M.; Kozin, F.; Carson, D.A.;  
J. Exp. Med. 175, 831-842, 1992  
A;Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from t  
A;Reference number: S23623; MUID:92156804; PMID:1740665  
A;Accession: S23628  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-111 <OLE>  
A;Cross-references: UNIPARC:UPI0000115F96; EMBL:X59705; NID:g34022; PIDN:CAA42226.1; PID  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 92.3%; Score 524.5; DB 2; Length 111;









A;Cross-references: UNIPARC:UPI0000115E41; EMBL:X17264; NID:g37898; PIDN:CAA35168.1; PID  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1989  
C;Genetics:  
A;Introns: 17/1  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;36-110/Domain: immunoglobulin homology <IMM>

Query Match 82.9%; Score 471; DB 2; Length 115;  
Best Local Similarity 96.8%; Pred. No. 4.3e-34;  
Matches 91; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYSLAWYQQKPGQAPRLLIYDASNRATGIPA 60  
Db 21 EIVLTQSPATLSLSPGERATLSCRASQGVSSYSLAWYQQKPGQAPRLLIYDASNRATGIPA 80

Qy 61 RFGSGSGTDFTLTISSLEPEDFAVYYCQQRSNW 94  
Db 81 RFGSGSGTDFTLTISSLEPEDFAVYYCQQRSNW 114

Search completed: December 28, 2005, 14:04:03  
Job time : 23.1538 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 28, 2005, 13:44:24 ; Search time 137.077 Seconds  
(without alignments)  
555.871 Million cell updates/sec

Title: US-09-920-137F-8  
Perfect score: 568  
Sequence: 1 EIVLTQSPATLSLSPGERAT.....QQRSNWPPFTFGPGTKVDIK 108

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_05.80:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB Length	ID	Description
1	487	85.7	115	1	KV3I1_HUMAN	P04433 homo sapien
2	479.5	84.4	108	2	Q9UL83_HUMAN	Q9ul83 homo sapien
3	474	83.5	129	1	KV3H_HUMAN	P04207 homo sapien
4	468	82.4	109	2	Q9UL85_HUMAN	Q9ul85 homo sapien
5	454	79.9	129	1	KV3L_HUMAN	P18135 homo sapien
6	453	79.8	109	1	KV3F_HUMAN	P1624 homo sapien
7	453	79.8	129	1	KV3M_HUMAN	P18136 homo sapien
8	449	79.0	109	2	Q9UL78_HUMAN	Q9ul78 homo sapien
9	448	78.9	109	1	KV3B_HUMAN	P01620 homo sapien
10	448	78.9	109	1	KV3D_HUMAN	P01622 homo sapien
11	448	78.9	109	2	Q9UL86_HUMAN	Q9ul86 homo sapien
12	447.5	78.8	236	2	Q6PIL8_HUMAN	Q6pil8 homo sapien
13	447	78.7	235	2	Q6PJF2_HUMAN	Q6pjf2 homo sapien
14	443.5	78.1	236	2	Q6P5S8_HUMAN	Q6p5s8 homo sapien
15	442	77.8	109	1	KV3E_HUMAN	P01623 homo sapien
16	442	77.8	235	2	Q6GMW0_HUMAN	Q6gmw0 homo sapien
17	431.5	76.0	128	1	KV3K_HUMAN	P06311 homo sapien
18	429	75.5	108	1	KV3A_HUMAN	P01619 homo sapien
19	428	75.4	109	1	KV3G_HUMAN	P04206 homo sapien
20	428	75.4	235	2	Q6GMV9_HUMAN	Q6gmv9 homo sapien
21	414.5	73.0	116	1	KV3J_HUMAN	P04434 homo sapien
22	411.5	72.4	100	1	KV3C_HUMAN	P01621 homo sapien
23	411.5	72.4	236	2	Q6GMX8_HUMAN	Q6gmx8 homo sapien
24	407.5	71.7	108	1	KV1M_HUMAN	P01605 homo sapien
25	401.5	70.7	244	2	Q65ZC8_HUMAN	Q65zc8 homo sapien
26	398	70.1	107	1	KV1D_HUMAN	P01596 homo sapien
27	397.5	70.0	108	1	KV1V_HUMAN	P04430 homo sapien
28	397.5	70.0	240	2	Q65ZC9_HUMAN	Q65zc9 homo sapien
29	396.5	69.8	236	2	Q6PIH7_HUMAN	Q6pih7 homo sapien
30	393.5	69.3	108	2	Q9UL79_HUMAN	Q9ul79 homo sapien
31	392	69.0	107	2	Q96SA9_HUMAN	Q96sa9 homo sapien

32	390.5	68.8	108	2	Q9UL77_HUMAN	Q9ul77 homo sapien
33	385.5	67.9	108	1	KV1H_HUMAN	P01600 homo sapien
34	385.5	67.9	234	2	Q569I9_HUMAN	Q569i9 homo sapien
35	385	67.8	107	2	Q9UL81_HUMAN	Q9ul81 homo sapien
36	384.5	67.7	111	1	KV3M_MOUSE	P01665 mus musculu
37	383.5	67.5	134	1	KV4C_HUMAN	P06314 homo sapien
38	382.5	67.3	108	1	KV1K_HUMAN	P01603 homo sapien
39	381.5	67.2	108	1	KV1L_HUMAN	P01604 homo sapien
40	380.5	67.0	111	1	KV3O_MOUSE	P01667 mus musculu
41	380.5	67.0	236	2	Q6GMW1_HUMAN	Q6gmw1 homo sapien
42	379.5	66.8	108	2	Q9UL70_HUMAN	Q9ul70 homo sapien
43	378.5	66.6	111	1	KV3L_MOUSE	P01664 mus musculu
44	377.5	66.5	108	1	KV1E_HUMAN	P01597 homo sapien
45	377.5	66.5	111	1	KV3H_MOUSE	P01660 mus musculu

ALIGNMENTS

RESULT 1  
KV3I1\_HUMAN  
ID KV3I1\_HUMAN STANDARD; PRT; 115 AA.  
AC P04433;  
DT 13-AUG-1987 (Rel. 05, Created)  
DT 13-AUG-1987 (Rel. 05, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Ig kappa chain V-III region VG precursor (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=85087932; PubMed=6440122;  
RA Pech M., Zachau H.G.;  
RT "Immunoglobulin genes of different subgroups are interdigitated within  
the VK locus.";  
RL Nucleic Acids Res. 12:9229-9236(1984).  
CC -----  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
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the European Bioinformatics Institute. There are no restrictions on its  
use as long as its content is in no way modified and this statement is not  
removed.  
CC -----  
CC EMBL; X01668; -, NOT\_ANNOTATED\_CDS; Genomic\_DNA.  
DR PIR; A01900; K3HUVG.  
DR HSSP; P01625; 1BEEQ.  
DR SMR; P04433; 21-115.  
DR GO; GO:0005576; C:extracellular region; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin domain; Immunoglobulin V region; Signal.  
FT SIGNAL 1 20  
FT CHAIN 21 >115 Ig kappa chain V-III region VG.  
FT REGION 21 43 Framework-1.  
FT REGION 44 54 Complementarity-determining-1.  
FT REGION 55 69 Framework-2.  
FT REGION 70 76 Complementarity-determining-2.  
FT REGION 77 108 Complementarity-determining-3.  
FT REGION 109 115 Complementarity-determining-3.  
FT DISULFID 43 108 By similarity.  
FT NON\_TER 115  
SQ SEQUENCE 115 AA; 12575 MW; 2DE47CDA3A17D555 CRC64;

Query Match 85.7%; Score 487; DB 1; Length 115;  
Best Local Similarity 98.9%; Pred. No. 9.5e-43;  
Matches 94; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQQKPGQAPRLLIYDASNRTATGIPA 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      21 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQQKPGQAPRLLIYDASNRTATGIPA 80
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY      61 RFSGSGSGTDFTLTISLSEPEDFAVYYCQQRSNWP 95
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      81 RFSGSGSGTDFTLTISLSEPEDFAVYYCQQRSNWP 115
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 2
Q9UL83 HUMAN
ID   Q9UL83_HUMAN PRELIMINARY;          PRT;   108 AA.
AC   Q9UL83;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Myosin-reactive immunoglobulin light chain variable region
     (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=98277139; PubMed=8436174;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
     fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=8436174;
RA   Wagner S.D., Luzzatto L.;
RT   "V kappa gene segments rearranged in chronic lymphocytic leukemia are
     distributed over a large portion of the V kappa locus and do not show
     somatic mutation.";
RL   Eur. J. Immunol. 23:391-397(1993).
DR   EMBL; AF035031; AAD56267.1; -; mRNA.
DR   PIR; B30609; B30609.
DR   PIR; C30609; C30609.
DR   PIR; D30609; D30609.
DR   PIR; S34098; S34098.
DR   PIR; S34099; S34099.
DR   HSSP; P01625; 1LVE.
DR   SMR; Q9UL83; 1-108.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGV; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER      1      108
FT   NON_TER      108   108
SQ   SEQUENCE 108 AA; 11834 MW; 9F9C5A92EBA96EEA CRC64;

Query Match      84.4%; Score 479.5; DB 2; Length 108;
Best Local Similarity 88.0%; Pred. No. 5.3e-42;
Matches 95; Conservative 5; Mismatches 7; Indels 1; Gaps 1;

QY      1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQQKPGQAPRLLIYDASNRTATGIPA 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      1 EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYCASTRATGIPA 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY      61 RFSGSGSGTDFTLTISLSEPEDFAVYYCQQRSNWPPTFGPGTKVDIK 108
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      61 RFSGSGSGTEFTLTISLQFEDFAVYYCQHYNW-PFTFGPGTKVDIK 107
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 3
KV3H_HUMAN
ID   KV3H_HUMAN          STANDARD;          PRT;   129 AA.
AC   P04207;
```

```
DT      20-MAR-1987 (Rel. 04, Created)
DT      01-NOV-1990 (Rel. 16, Last sequence update)
DT      10-MAY-2005 (Rel. 47, Last annotation update)
DE      Ig kappa chain V-III region CLL precursor (Rheumatoid factor).
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC      Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RX      MEDLINE=86177570; PubMed=3083417;
RA      Jirik F.R., Sorge J., Fong S., Heitzmann J.G., Curd J.G., Chen P.P.,
RA      Goldfien R., Carson D.A.;
RT      "Cloning and sequence determination of a human rheumatoid factor
     light-chain gene.";
RT      light-chain gene.";
RL      Proc. Natl. Acad. Sci. U.S.A. 83:2195-2199(1986).
CC      -----
CC      This Swiss-Prot entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use as long as its content is in no way modified and this statement is not
CC      removed.
CC      -----
DR      EMBL; M12740; AAA58992.1; -; Genomic_DNA.
DR      HSSP; P01625; 1LVE.
DR      SMR; P04207; 21-129.
DR      GO; GO:0005576; C:extracellular region; NAS.
DR      GO; GO:0003823; F:antigen binding; NAS.
DR      GO; GO:0006955; P:immune response; NAS.
DR      InterPro; IPR007110; Ig-like.
DR      InterPro; IPR003596; Ig_v.
DR      SMART; SM00406; IGV; 1.
DR      PROSITE; PS50835; IG_LIKE; 1.
KW      Immunoglobulin domain; Immunoglobulin V region; Signal.
FT   SIGNAL      1      20
FT   CHAIN      21     129   Ig kappa chain V-III region CLL.
FT   REGION     21     43   Framework-1.
FT   REGION     44     54   Complementarity-determining-1.
FT   REGION     55     69   Framework-2.
FT   REGION     70     76   Complementarity-determining-2.
FT   REGION     77     108  Framework-3.
FT   REGION     109    118  Complementarity-determining-3.
FT   REGION     119    129  JK1 segment.
FT   DISULFID    43     108  By similarity.
FT   NON_TER     129    129
SQ   SEQUENCE 129 AA; 14275 MW; 5C13B411BE60CC14 CRC64;

Query Match      83.5%; Score 474; DB 1; Length 129;
Best Local Similarity 83.3%; Pred. No. 2.5e-41;
Matches 90; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY      1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQQKPGQAPRLLIYDASNRTATGIPA 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      21 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQQKPGQPPRLLIYGASTRATGIPA 80
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY      61 RFSGSGSGTDFTLTISLSEPEDFAVYYCQQRSNWPPTFGPGTKVDIK 108
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      81 RFSGSGSGTEFTLTISRLQSEDFAVYYCQQYNNWPDWTFGQGRVEIK 128
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 4
Q9UL85_HUMAN
ID   Q9UL85_HUMAN PRELIMINARY;          PRT;   109 AA.
AC   Q9UL85;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Myosin-reactive immunoglobulin kappa chain variable region
     (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
```



FT NON\_TER 109 109  
SQ SEQUENCE 109 AA; 11922 MW; 62821DDC6A8ABA86 CRC64;

Query Match 79.8%; Score 453; DB 1; Length 109;  
Best Local Similarity 81.7%; Pred. No. 3.1e-39;  
Matches 89; Conservative 9; Mismatches 9; Indels 2; Gaps 2;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSV-YSYLAWYQOKPGQAPRLLIYDASNRATGIP 59  
Db 1 EIVMTQSPVTLSPGERATLSCRASQSI NSYLAWYQOKPGSGPRLLIYGASTRATGIP 60

Qy 60 ARFSGSGGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPTKVDIK 108  
Db 61 ARFSGSGGTEFTLTISSLQSEDFAVYYCQQYNNWPP-TFGQGRVEIK 108

RESULT 7  
KV3M\_HUMAN STANDARD; PRT; 129 AA.  
AC P18136;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Ig kappa chain V-III region HIC precursor.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=88171307; PubMed=3127527; DOI=10.1084/jem.167.3.840;  
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;  
RT "Autoantibody-associated kappa light chain variable region gene expressed in chronic lymphocytic leukemia with little or no somatic mutation. Implications for etiology and immunotherapy.";  
RL J. Exp. Med. 167:840-852(1988).  
CC -!- DISEASE: The protein is one of the surface immunoglobulin M autoantibodies expressed in patients with chronic lymphocytic leukemia.  
CC -----  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.  
CC -----  
DR PIR; P10021; K3HUHI.  
DR HSSP; P01625; IEEQ.  
DR SMR; P18136; 21-129.  
DR Ensembl; ENSG00000169769; Homo sapiens.  
DR GO; GO:0005576; C:extracellular region; NAS.  
DR GO; GO:0003823; F:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin domain; Immunoglobulin V region; Signal.  
FT SIGNAL 1 20  
FT CHAIN 21 129 Ig kappa chain V-III region HIC.  
FT REGION 21 43 Framework-1.  
FT REGION 44 55 Complementarity-determining-1.  
FT REGION 56 70 Framework-2.  
FT REGION 71 77 Complementarity-determining-2.  
FT REGION 78 109 Framework-3.  
FT REGION 110 118 Complementarity-determining-3.  
FT REGION 119 129 JK1 segment.  
FT DISULFID 43 109 By similarity.  
FT NON\_TER 129 129  
SQ SEQUENCE 129 AA; 14071 MW; 7395528EA2BB74D6 CRC64;

Query Match 79.8%; Score 453; DB 1; Length 129;

Best Local Similarity 85.3%; Pred. No. 3.8e-39;  
Matches 93; Conservative 4; Mismatches 10; Indels 2; Gaps 2;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSV-YSYLAWYQOKPGQAPRLLIYDASNRATGIP 59  
Db 21 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQOKPGQAPRLLIYGASSRATGIP 80

Qy 60 ARFSGSGGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPTKVDIK 108  
Db 81 DRFSGSGGTDFTLTISRLEPXDFAVYYCQYCS-SPWTFGQGTKVEIK 128

RESULT 8  
Q9UL78\_HUMAN PRELIMINARY; PRT; 109 AA.  
AC Q9UL78;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Myosin-reactive immunoglobulin light chain variable region (Fragment).  
DE (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus.";  
RT Clin. Immunol. Immunopathol. 87:184-192(1998).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=1373487;  
RA Zebedee S.L., Barbas C.F. 3rd, Hom Y.L., Caothien R.H., Graff R.,  
RA DeGraw J., Pyati J., LaPolla R., Burton D.R., Lerner R.A.;  
RT "Human combinatorial antibody libraries to hepatitis B surface antigen.";  
RT Proc. Natl. Acad. Sci. U.S.A. 89:3175-3179(1992).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=8436174;  
RA Wagner S.D., Luzzatto L.;  
RT "V kappa gene segments rearranged in chronic lymphocytic leukemia are distributed over a large portion of the V kappa locus and do not show somatic mutation.";  
RT Eur. J. Immunol. 23:391-397(1993).  
RN [4]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=1552291;  
RA Martin T., Duffy S.F., Carson D.A., Kipps T.J.;  
RT "Evidence for somatic selection of natural autoantibodies.";  
RL J. Exp. Med. 175:983-991(1992).  
DR EMBL; AF035036; AAD56272.1; -; mRNA.  
DR PIR; A30601; A30601.  
DR PIR; A30608; A30608.  
DR PIR; B30601; B30601.  
DR PIR; B30607; B30607.  
DR PIR; C30601; C30601.  
DR PIR; C30607; C30607.  
DR PIR; C30608; C30608.  
DR PIR; D30601; D30601.  
DR PIR; D30607; D30607.  
DR PIR; D30608; D30608.  
DR PIR; F30607; F30607.  
DR PIR; F30608; F30608.  
DR PIR; G30601; G30601.  
DR PIR; G30608; G30608.  
DR PIR; H30607; H30607.  
DR PIR; H30608; H30608.



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DR  PIR; H44151; H44151.
DR  PIR; I30601; I30601.
DR  PIR; PH0963; PH0963.
DR  PIR; PH0964; PH0964.
DR  PIR; PH0965; PH0965.
DR  PIR; S33988; S33988.
DR  PIR; S34096; S34096.
DR  HSSP; P01625; 1EK3.
DR  SMR; Q9UL78; 1-109.
DR  InterPro; IPR007110; Ig-like.
DR  InterPro; IPR003596; Ig_v.
DR  SMART; SM00406; IGV; 1.
DR  PROSITE; PS50835; IG_LIKE; 1.
FT  NON_TER 1 109
FT  NON_TER 109
SQ  SEQUENCE 109 AA; 11646 MW; 5F675C52EC7EE197 CRC64;

Query Match      79.0%; Score 449; DB 2; Length 109;
Best Local Similarity 85.3%; Pred. No. 8.1e-39;
Matches 93; Conservative 3; Mismatches 11; Indels 2; Gaps 2;

QY  1 EIVLTQSPATLSLSPGERATLSCRASQSV-YSYLAWYQOKPGQAPRLLIYDASNRATGIP 59
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Db  1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQOKPGQAPRLLIYGASSRATGIP 60

QY  60 ARFSGSGGTDFTLTISLSEPEDFAVYQCQRSNWPPFTFGPGTKVDIK 108
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Db  61 DRFSGSGGTDFTLTISRLEPDCAVYCCQYGS-SPLTFGGGTVKVEIK 108

RESULT 9
KV3B_HUMAN
ID  KV3B_HUMAN STANDARD; PRT; 109 AA.
AC  P01620;
DT  21-JUL-1986 (Rel. 01, Created)
DT  21-JUL-1986 (Rel. 01, Last sequence update)
DT  10-MAY-2005 (Rel. 47, Last annotation update)
DE  Ig kappa chain V-III region SIE.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC  Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  PROTEIN SEQUENCE.
RX  MEDLINE=82046598; PubMed=6794615;
RA  Andrews D.W., Capra J.D.;
RT  "Amino acid sequence of the variable regions of light chains from two
RT  idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
RT  group.";
RL  Biochemistry 20:5816-5822(1981).
CC  -!- MISCELLANEOUS: This chain was isolated from an IgM with anti-gamma
CC  globulin activity.
CC  -----
CC  This Swiss-Prot entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use as long as its content is in no way modified and this statement is not
CC  removed.
CC  -----
DR  PIR; A01892; K3HUSI.
DR  HSSP; P01625; 1LVE.
DR  SMR; P01620; 1-109.
DR  GO; GO:0005576; C:extracellular region; NAS.
DR  GO; GO:0003823; F:antigen binding; NAS.
DR  GO; GO:0006955; P:immune response; NAS.
DR  InterPro; IPR007110; Ig-like.
DR  InterPro; IPR003596; Ig_v.
DR  SMART; SM00406; IGV; 1.
DR  PROSITE; PS50835; IG_LIKE; 1.
KW  Direct protein sequencing; Immunoglobulin domain;
KW  Immunoglobulin V region.
FT  DISULFID 23 89 By similarity.
SQ  SEQUENCE 109 AA; 11646 MW; 5F675C52EC7EE197 CRC64;
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FT  NON_TER 109 109
SQ  SEQUENCE 109 AA; 11775 MW; 7689C3ECD646FFB4 CRC64;

Query Match      78.9%; Score 448; DB 1; Length 109;
Best Local Similarity 84.4%; Pred. No. 1e-38;
Matches 92; Conservative 5; Mismatches 10; Indels 2; Gaps 2;

QY  1 EIVLTQSPATLSLSPGERATLSCRASQSV-YSYLAWYQOKPGQAPRLLIYDASNRATGIP 59
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Db  1 EIVLTQSPGTLSLSPGERATLSCRASQSVNSYLAWYQOKPGQAPRLLIYGASSRATGIP 60

QY  60 ARFSGSGGTDFTLTISLSEPEDFAVYQCQRSNWPPFTFGPGTKVDIK 108
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db  61 DRFSGSGGTDFTLTISRLEPDDFAVYCCQYGS-SPQTFGGGSKVEIK 108

RESULT 10
KV3D_HUMAN
ID  KV3D_HUMAN STANDARD; PRT; 109 AA.
AC  P01622;
DT  21-JUL-1986 (Rel. 01, Created)
DT  21-JUL-1986 (Rel. 01, Last sequence update)
DT  10-MAY-2005 (Rel. 47, Last annotation update)
DE  Ig kappa chain V-III region Ti.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC  Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  PROTEIN SEQUENCE.
RX  MEDLINE=72188439; PubMed=5027703;
RA  Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;
RT  "Rule of antibody structure. The primary structure of a monoclonal
RT  immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein
RT  Ti). IV. The complete amino acid sequence and its significance for the
RT  mechanism of antibody production.";
RL  Hoppe-Seyleyler's Z. Physiol. Chem. 353:189-208(1972).
CC  -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC  -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC  -----
CC  This Swiss-Prot entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use as long as its content is in no way modified and this statement is not
CC  removed.
CC  -----
DR  PIR; A01895; K3HUTI.
DR  HSSP; P01625; 1LVE.
DR  SMR; P01622; 1-109.
DR  GO; GO:0005576; C:extracellular region; NAS.
DR  GO; GO:0003823; F:antigen binding; NAS.
DR  GO; GO:0006955; P:immune response; NAS.
DR  InterPro; IPR007110; Ig-like.
DR  InterPro; IPR003596; Ig_v.
DR  SMART; SM00406; IGV; 1.
DR  PROSITE; PS50835; IG_LIKE; 1.
KW  Bence-Jones protein; Direct protein sequencing; Immunoglobulin domain;
KW  Immunoglobulin V region.
FT  DISULFID 23 89 By similarity.
FT  NON_TER 109 109
SQ  SEQUENCE 109 AA; 11788 MW; 8C35058CDC7749BC CRC64;

Query Match      78.9%; Score 448; DB 1; Length 109;
Best Local Similarity 84.4%; Pred. No. 1e-38;
Matches 92; Conservative 5; Mismatches 10; Indels 2; Gaps 2;

QY  1 EIVLTQSPATLSLSPGERATLSCRASQSV-YSYLAWYQOKPGQAPRLLIYDASNRATGIP 59
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db  1 EIVLTQSPGTLSLSPGERATLSCRASQSVNSFLAWYQOKPGQAPRLLIYVASSRATGIP 60

QY  60 ARFSGSGGTDFTLTISLSEPEDFAVYQCQRSNWPPFTFGPGTKVDIK 108
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
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Db 61 DRFSGSGGTDFTLTISRLEPEDFAVYYCQYGS-SPSTFGQGTKVELK 108

RESULT 11

Q9UL86 HUMAN

ID Q9UL86 HUMAN PRELIMINARY; PRT; 109 AA.

AC Q9UL86;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Myosin-reactive immunoglobulin kappa chain variable region (Fragment).

DE (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;

RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;

RA "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus.";

RT Clin. Immunol. Immunopathol. 87:184-192(1998).

RL EMBL; AF035028; AAD56264.1; -; mRNA.

DR PIR; B30607; B30607.

DR PIR; I30601; I30601.

DR HSSP; P01625; 1EK3.

DR SMR; Q9UL86; 1-109.

DR Ensembl; ENSG00000169769; Homo sapiens.

DR InterPro; IPR007110; IG-like.

DR InterPro; IPR003596; IG\_v.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG\_LIKE; 1.

FT NON\_TER 1 109

FT NON\_TER 109 109

SQ SEQUENCE 109 AA; 11928 MW; 243325F72C7DAC83 CRC64;

Query Match 78.9%; Score 448; DB 2; Length 109;

Best Local Similarity 85.3%; Pred. No. 1e-38;

Matches 93; Conservative 2; Mismatches 12; Indels 2; Gaps 2;

QY 1 EIVLTQSPATLSLSPGERATLSCRASQSV-YSYLAWYQQKPGQAPRLLIYDASNRATGIP 59

Db 1 EIVLTQSPGTLSPFGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGTSSRATGIP 60

QY 60 ARFSGSGGTDFTLTISRLEPEDFAVYYCQQRSNWPPFTFGPTKVDIK 108

Db 61 DRFSGSGSETDFTLTISRLEPEDFAVYYCQYGS-SIFTFGPTKVDIK 108

RESULT 12

Q6PIL8 HUMAN

ID Q6PIL8 HUMAN PRELIMINARY; PRT; 236 AA.

AC Q6PIL8;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Hypothetical protein.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RL [2]

RN NUCLEOTIDE SEQUENCE.

RP TISSUE=Brain;

RC Strausberg R.;

RA Submitted (JUN-2002) to the EMBL/GenBank/DBBJ databases.

RL EMBL; BC032451; AAH32451.1; -; mRNA.

DR HSSP; P01837; 1KCU.

DR SMR; Q6PIL8; 21-236.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003597; Ig\_c1.

DR InterPro; IPR003006; Ig\_MHC.

DR InterPro; IPR003596; Ig\_v.

DR Pfam; PF07654; C1-set; 1.

DR SMART; SM00409; IG; 2.

DR SMART; SM00407; IGC1; 1.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG\_LIKE; 2.

DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.

KW Hypothetical protein.

SQ SEQUENCE 236 AA; 25834 MW; 6647A9E77A3C0053 CRC64;

Query Match 78.8%; Score 447.5; DB 2; Length 236;

Best Local Similarity 82.6%; Pred. No. 2.9e-38;

Matches 90; Conservative 4; Mismatches 14; Indels 1; Gaps 1;

QY 1 EIVLTQSPATLSLSPGERATLSCRASQSV-YSYLAWYQQKPGQAPRLLIYDASNRATGIP 59

Db 21 ENVLTQSPGTLSPGERATLSCRASQSLSSSYLAWYQQKPGQAPRLLIYGVSSRATGIP 80

QY 60 ARFSGSGGTDFTLTISRLEPEDFAVYYCQQRSNWPPFTFGPTKVDIK 108

Db 81 DRFSGSGGTDFTLTISRLEPEDFAVYYCQYGTSRPITFGQTRLDIK 129

RESULT 13

Q6PJF2 HUMAN

ID Q6PJF2 HUMAN PRELIMINARY; PRT; 235 AA.

AC Q6PJF2;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Hypothetical protein.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Lung;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 28, 2005, 13:53:15 ; Search time 30 Seconds  
(without alignments)  
297.632 Million cell updates/sec

Title: US-09-920-137F-8  
Perfect score: 568  
Sequence: 1 EIVLTQSPATLSLSPGERAT.....QQRSNWPPFTFGPGTKVDIK 108

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents,AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/iaa/6\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/H\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/RE\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	523.5	92.2	224	2	US-09-456-090A-46
2	523.5	92.2	224	2	US-09-453-234-46
3	522.5	92.0	107	2	US-09-434-870-2
4	518.5	91.3	224	2	US-09-456-090A-82
5	518.5	91.3	224	2	US-09-456-090A-88
6	518.5	91.3	224	2	US-09-456-090A-90
7	518.5	91.3	224	2	US-09-453-234-82
8	518.5	91.3	224	2	US-09-453-234-88
9	518.5	91.3	224	2	US-09-453-234-90
10	517.5	91.1	224	2	US-09-456-090A-36
11	517.5	91.1	224	2	US-09-453-234-36
12	514.5	90.6	224	2	US-09-456-090A-84
13	514.5	90.6	224	2	US-09-453-234-84
14	509.5	89.7	107	2	US-09-438-954-40
15	493.5	86.9	226	2	US-09-456-090A-38
16	493.5	86.9	226	2	US-09-453-234-38
17	491.5	86.5	234	2	US-09-848-832-4
18	489	86.1	105	2	US-08-635-109-6
19	489	86.1	105	2	US-08-844-215-9
20	489	86.1	117	2	US-09-203-768A-4
21	487	85.7	95	2	US-10-194-975-86
22	487	85.7	115	1	US-08-053-131-179
23	487	85.7	115	1	US-08-096-762-179
24	487	85.7	115	2	US-09-042-353-42
25	487	85.7	115	2	US-08-758-417A-307
26	485.5	85.5	226	2	US-09-456-090A-72
27	485.5	85.5	226	2	US-09-453-234-72

28	479.5	84.4	226	2	US-09-456-090A-42	Sequence 42, Appl
29	479.5	84.4	226	2	US-09-453-234-42	Sequence 42, Appl
30	474	83.5	110	2	US-09-025-769B-30	Sequence 30, Appl
31	474	83.5	110	2	US-09-025-769B-47	Sequence 47, Appl
32	474	83.5	110	2	US-09-490-070A-30	Sequence 30, Appl
33	474	83.5	110	2	US-09-490-070A-47	Sequence 47, Appl
34	474	83.5	110	2	US-09-490-153-30	Sequence 30, Appl
35	474	83.5	110	2	US-09-490-153-47	Sequence 47, Appl
36	474	83.5	110	2	US-09-490-324-30	Sequence 30, Appl
37	474	83.5	110	2	US-09-490-324-47	Sequence 47, Appl
38	473.5	83.4	226	2	US-09-456-090A-50	Sequence 50, Appl
39	473.5	83.4	226	2	US-09-456-090A-86	Sequence 86, Appl
40	473.5	83.4	226	2	US-09-453-234-50	Sequence 50, Appl
41	473.5	83.4	226	2	US-09-453-234-86	Sequence 86, Appl
42	472.5	83.2	226	2	US-09-456-090A-74	Sequence 74, Appl
43	472.5	83.2	226	2	US-09-453-234-74	Sequence 74, Appl
44	471.5	83.0	234	2	US-09-472-087-17	Sequence 17, Appl
45	471.5	83.0	234	2	US-09-472-087-69	Sequence 69, Appl

ALIGNMENTS

RESULT 1  
US-09-456-090A-46  
; Sequence 46, Application US/09456090A  
; Patent No. 6680209  
; GENERAL INFORMATION:  
; APPLICANT: Buechler, Joe  
; APPLICANT: Valkirs, Gunars  
; APPLICANT: Gray, Jeff  
; APPLICANT: Lonberg, Nils  
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS  
; FILE REFERENCE: 020015-000200US  
; CURRENT APPLICATION NUMBER: US/09/456,090A  
; CURRENT FILING DATE: 1999-12-06  
; NUMBER OF SEQ ID NOS: 110  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 46  
; LENGTH: 224  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; OTHER INFORMATION: M1-10L  
US-09-456-090A-46

Query Match	92.2%	Score	523.5;	DB	2;	Length	224;
Best Local Similarity	93.5%;	Pred. No.	2e-42;	Mismatches	4;	Indels	1;
Matches	101;	Conservative	4;	2;	Gaps	1;	
QY	1	EIVLTQSPATLSLSPGERATLS	CRASQSVSYLA	WYQKPGQAPRL	LIYDASNRATG	IPA	60
Db	1	DVVMTQSPATLSLSPGERATLS	CRASQSVSSYLA	WYQKPGQAPRL	LIYDASNRATG	IPA	60
QY	61	RFSGSGSGTDFTLTITSSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK					108
Db	61	RFSGSGSGTDFTLTITSSLEPEDFAVYYCQQRSNWPP-TFGGGTKVEIK					107

RESULT 2  
US-09-453-234-46  
; Sequence 46, Application US/09453234  
; Patent No. 6794132  
; GENERAL INFORMATION:  
; APPLICANT: Buechler, Joe  
; APPLICANT: Valkirs, Gunars  
; APPLICANT: Gray, Jeff  
; APPLICANT: Lonberg, Nils  
; APPLICANT: Biosite Diagnostics, Inc.  
; APPLICANT: Genpharm International  
; TITLE OF INVENTION: Human Antibodies  
; FILE REFERENCE: 020015-000110US  
; CURRENT APPLICATION NUMBER: US/09/453,234  
; CURRENT FILING DATE: 1999-12-01

```
; PRIOR APPLICATION NUMBER: US 60/157,415
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M1-10L
US-09-453-234-46

Query Match      92.2%; Score 523.5; DB 2; Length 224;
Best Local Similarity 93.5%; Pred. No. 2e-42;
Matches 101; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

QY      1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
      ::::|||||
Db      1 DVVMTQSPATLSLSPGERATLSCRASQSVSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
      ::::|||||

QY      61 RFSGSGGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
      |||||
Db      61 RFSGSGGTDFTLTISSLEPEDFAVYYCQQRSNWPP-TFGGGTKVEIK 107

RESULT 3
US-09-434-870-2
; Sequence 2, Application US/09434870
; Patent No. 6849425
; GENERAL INFORMATION:
; APPLICANT: Huse, William
; APPLICANT: Watkins, Jeffry
; APPLICANT: Wu, Herren
; TITLE OF INVENTION: Methods of Optimizing Antibody Variable Region Binding Affinity
; FILE REFERENCE: AME-06352
; CURRENT APPLICATION NUMBER: US/09/434,870
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/159,689
; PRIOR FILING DATE: 1999-10-14
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-434-870-2

Query Match      92.0%; Score 522.5; DB 2; Length 107;
Best Local Similarity 95.4%; Pred. No. 1.1e-42;
Matches 103; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY      1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
      |||||
Db      1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
      |||||

QY      61 RFSGSGGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
      |||||
Db      61 RFSGSGGTDFTLTISSLEPEDFAVYYCQQRSNW-PLTFGGGTKVEIK 107

RESULT 4
US-09-456-090A-82
; Sequence 82, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 82
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-31L
US-09-456-090A-82

Query Match      91.3%; Score 518.5; DB 2; Length 224;
Best Local Similarity 94.4%; Pred. No. 6e-42;
Matches 102; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY      1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
      |||||
Db      1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
      |||||

QY      61 RFSGSGGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
      |||||
Db      61 RFSGSGGTDFTLTISSLEPEDFAVYYCQQRTNWPR-TFGQGTKVEIK 107

RESULT 5
US-09-456-090A-88
; Sequence 88, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 88
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-34L
US-09-456-090A-88

Query Match      91.3%; Score 518.5; DB 2; Length 224;
Best Local Similarity 94.4%; Pred. No. 6e-42;
Matches 102; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY      1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
      |||||
Db      1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
      |||||

QY      61 RFSGSGGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
      |||||
Db      61 RFSGSGGTDFTLTISSLEPEDFAVYYCQQRTNWPR-TFGQGTKVEIK 107

RESULT 6
US-09-456-090A-90
; Sequence 90, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 90
; LENGTH: 224
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; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-35L
US-09-456-090A-90

Query Match          91.3%; Score 518.5; DB 2; Length 224;
Best Local Similarity 94.4%; Pred. No. 6e-42;
Matches 102; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYSLAWYQQKPGQAPRLLIYDASNRATGIPA 60
   |||||
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYSLAWYQQKPGQAPRLLIYDASNRATGIPA 60

Qy 61 RFSGSGGTDFTLTISSLEPEDFAVYQCQRSNWPPFTFGPGTKVDIK 108
   |||||
Db 61 RFSGSGGTDFTLTISSLEPEDFAVYCCQRTNWPR-TFGQGTKVEIK 107

RESULT 7
US-09-453-234-82
; Sequence 82, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: GenPharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453,234
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/157,415
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 82
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-31L
US-09-453-234-82

Query Match          91.3%; Score 518.5; DB 2; Length 224;
Best Local Similarity 94.4%; Pred. No. 6e-42;
Matches 102; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYSLAWYQQKPGQAPRLLIYDASNRATGIPA 60
   |||||
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYSLAWYQQKPGQAPRLLIYDASNRATGIPA 60

Qy 61 RFSGSGGTDFTLTISSLEPEDFAVYQCQRSNWPPFTFGPGTKVDIK 108
   |||||
Db 61 RFSGSGGTDFTLTISSLEPEDFAVYCCQRTNWPR-TFGQGTKVEIK 107

RESULT 8
US-09-453-234-88
; Sequence 88, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: GenPharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453,234
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/157,415
; 
```

```
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 88
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-34L
US-09-453-234-88

Query Match          91.3%; Score 518.5; DB 2; Length 224;
Best Local Similarity 94.4%; Pred. No. 6e-42;
Matches 102; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYSLAWYQQKPGQAPRLLIYDASNRATGIPA 60
   |||||
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYSLAWYQQKPGQAPRLLIYDASNRATGIPA 60

Qy 61 RFSGSGGTDFTLTISSLEPEDFAVYQCQRSNWPPFTFGPGTKVDIK 108
   |||||
Db 61 RFSGSGGTDFTLTISSLEPEDFAVYCCQRTNWPR-TFGQGTKVEIK 107

RESULT 9
US-09-453-234-90
; Sequence 90, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: GenPharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453,234
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/157,415
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 90
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-35L
US-09-453-234-90

Query Match          91.3%; Score 518.5; DB 2; Length 224;
Best Local Similarity 94.4%; Pred. No. 6e-42;
Matches 102; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYSLAWYQQKPGQAPRLLIYDASNRATGIPA 60
   |||||
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYSLAWYQQKPGQAPRLLIYDASNRATGIPA 60

Qy 61 RFSGSGGTDFTLTISSLEPEDFAVYQCQRSNWPPFTFGPGTKVDIK 108
   |||||
Db 61 RFSGSGGTDFTLTISSLEPEDFAVYCCQRTNWPR-TFGQGTKVEIK 107

RESULT 10
US-09-456-090A-36
; Sequence 36, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; 
```

```

; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: M1-1L
US-09-456-090A-36

Query Match          91.1%; Score 517.5; DB 2; Length 224;
Best Local Similarity 94.4%; Pred. No. 7.5e-42;
Matches 102; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

QY 1 EIVLTQSPATLSLSPGERATLSCRASQSVYSYLAWYQQKPGQAPRLLIYDASNRAATGIPA 60
   |||||
Db 1 EIVLTQSPATLSLSPGERATLSCRASQGVSSYLAWYQQKPGQAPRLLIYDASNRAATGIPA 60

QY 61 RFSGSGSGTDFTLTISLSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
   |||||
Db 61 RFSGSGSGTDFTLTISLSLEPEDFAVYYCQQRSNWPR-TFGQGTKVEIK 107

RESULT 11
US-09-453-234-36
; Sequence 36, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: GenPharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453,234
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/157,415
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-453-234-36

Query Match          91.1%; Score 517.5; DB 2; Length 224;
Best Local Similarity 94.4%; Pred. No. 7.5e-42;
Matches 102; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

QY 1 EIVLTQSPATLSLSPGERATLSCRASQSVYSYLAWYQQKPGQAPRLLIYDASNRAATGIPA 60
   |||||
Db 1 EIVLTQSPATLSLSPGERATLSCRASQGVSSYLAWYQQKPGQAPRLLIYDASNRAATGIPA 60

QY 61 RFSGSGSGTDFTLTISLSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
   |||||
Db 61 RFSGSGSGTDFTLTISLSLEPEDFAVYYCQQRSNWPR-TFGQGTKVEIK 107

RESULT 12
US-09-456-090A-84
; Sequence 84, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
```

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; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 84
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-32L
US-09-456-090A-84

Query Match          90.6%; Score 514.5; DB 2; Length 224;
Best Local Similarity 93.5%; Pred. No. 1.4e-41;
Matches 101; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

QY 1 EIVLTQSPATLSLSPGERATLSCRASQSVYSYLAWYQQKPGQAPRLLIYDASNRAATGIPA 60
   |||||
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRAAGIPA 60

QY 61 RFSGSGSGTDFTLTISLSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
   |||||
Db 61 RFSGSGSGTDFTLTISLSLEPEDFAVYYCQQRNNW-PLTFGGGTTKVEIK 107

RESULT 13
US-09-453-234-84
; Sequence 84, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: GenPharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453,234
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/157,415
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 84
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-32L
US-09-453-234-84

Query Match          90.6%; Score 514.5; DB 2; Length 224;
Best Local Similarity 93.5%; Pred. No. 1.4e-41;
Matches 101; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

QY 1 EIVLTQSPATLSLSPGERATLSCRASQSVYSYLAWYQQKPGQAPRLLIYDASNRAATGIPA 60
   |||||
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRAAGIPA 60

QY 61 RFSGSGSGTDFTLTISLSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
   |||||
Db 61 RFSGSGSGTDFTLTISLSLEPEDFAVYYCQQRNNW-PLTFGGGTTKVEIK 107

RESULT 14
US-09-438-954-40
; Sequence 40, Application US/09438954
; Patent No. 6458934
; GENERAL INFORMATION:
; APPLICANT: HONG, Hyo Jeong
; APPLICANT: PARK, Sung Sup
; APPLICANT: KANG, Young Jun
; APPLICANT: KANG, Chang-Yuil
```

; APPLICANT: YOON, Sung Kwan  
; TITLE OF INVENTION: HUMANIZED ANTIBODY SPECIFIC FOR HUMAN 4-1BB AND  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION COMPRISING SAME  
; FILE REFERENCE: 1303-124P  
; CURRENT APPLICATION NUMBER: US/09/438,954  
; CURRENT FILING DATE: 1999-11-12  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 40  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Variable  
; OTHER INFORMATION: region of light chain of human antibody (X82934)  
US-09-438-954-40

Query Match 89.7%; Score 509.5; DB 2; Length 107;  
Best Local Similarity 90.7%; Pred. No. 1.9e-41;  
Matches 98; Conservative 5; Mismatches 4; Indels 1; Gaps 1;  
  
Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQQKPGQAPRLLIYDASNRRATGIPA 60  
  :::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 1 DVVMTQSPATLSVSPGERATLSCRASQSVSYLAWYQQKPGQAPRLLIYDASRRATGIPA 60  
  
Qy 61 RFGSGSGTDFTLTISLLEPEDFAVYQCQRSNWPPFTFGPGTKVDIK 108  
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 61 RFGSGSGTDFTLTISLLEPEDFAVYQCQRSNWPPPLTFGGTKVEIK 107

RESULT 15  
US-09-456-090A-38  
; Sequence 38, Application US/09456090A  
; Patent No. 6680209  
; GENERAL INFORMATION:  
; APPLICANT: Buechler, Joe  
; APPLICANT: Valkirs, Gunars  
; APPLICANT: Gray, Jeff  
; APPLICANT: Lonberg, Nils  
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS  
; FILE REFERENCE: 020015-000200US  
; CURRENT APPLICATION NUMBER: US/09/456,090A  
; CURRENT FILING DATE: 1999-12-06  
; NUMBER OF SEQ ID NOS: 110  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 38  
; LENGTH: 226  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; OTHER INFORMATION: M1-3L  
US-09-456-090A-38

Query Match 86.9%; Score 493.5; DB 2; Length 226;  
Best Local Similarity 89.9%; Pred. No. 1.5e-39;  
Matches 98; Conservative 3; Mismatches 7; Indels 1; Gaps 1;  
  
Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSV-YSYLAWYQQKPGQAPRLLIYDASNRRATGIP 59  
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 1 EIVMTQSPATLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRRATGIP 60  
  
Qy 60 ARFSGSGGTDFTLTISSLEPEDFAVYCCQRSNWPPFTFGPGTKVDIK 108  
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 61 DRFSGSGGTDFTLTISSLEPEDFAVYCCQYGSSPPFTFGPGTKVDIK 109

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OM protein - protein search, using sw model

Run on: December 28, 2005, 14:03:21 ; Search time 102.462 Seconds  
(without alignments)  
440.415 Million cell updates/sec

Title: US-09-920-137F-8  
Perfect score: 568  
Sequence: 1 EIVLTQSPATLSLSPGERAT.....QQRSNWPPFTFGPGTKVDIK 108

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA Main:  
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4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	559	98.4	108	4	US-10-305-347A-8
3	559	98.4	108	4	US-10-720-323-8
4	559	98.4	108	5	US-10-954-900A-8
5	541	95.2	108	6	US-11-009-731-90
6	541	95.2	109	4	US-10-408-901-24
7	541	95.2	215	4	US-10-408-901-48
8	540	95.1	128	4	US-10-656-769-12
9	540	95.1	130	4	US-10-394-471B-16
10	540	95.1	235	4	US-10-656-769-38
11	539	94.9	109	4	US-10-408-901-8
12	539	94.9	215	4	US-10-408-901-32
13	538	94.7	108	4	US-10-173-551-9
14	536	94.4	108	5	US-10-886-838-4
15	535	94.2	108	6	US-11-021-715-101
16	534	94.0	108	6	US-11-009-731-85
17	534	94.0	108	6	US-11-102-403-9
18	534	94.0	108	6	US-11-102-403-11
19	534	94.0	109	4	US-10-408-901-16
20	534	94.0	109	4	US-10-408-901-28
21	534	94.0	215	4	US-10-408-901-40
22	534	94.0	215	4	US-10-408-901-52
23	531.5	93.6	129	4	US-10-478-056-19
24	529.5	93.2	107	4	US-10-251-085B-142
25	529.5	93.2	107	4	US-10-737-252-142
26	529.5	93.2	236	5	US-10-961-567A-6
27	529	93.1	251	3	US-09-880-748-1049

28	529	93.1	251	4	US-10-293-418-1049	Sequence 1049, Ap
29	524.5	92.3	107	5	US-10-891-658-91	Sequence 91, Appl
30	524	92.3	108	5	US-10-886-838-2	Sequence 2, Appli
31	524	92.3	108	6	US-11-009-731-92	Sequence 92, Appl
32	523.5	92.2	107	3	US-09-791-153A-69	Sequence 69, Appl
33	523.5	92.2	224	3	US-09-453-234-46	Sequence 46, Appl
34	523	92.1	108	4	US-10-173-551-19	Sequence 19, Appl
35	523	92.1	130	4	US-10-443-466A-25	Sequence 25, Appl
36	522.5	92.0	107	3	US-09-791-153A-71	Sequence 71, Appl
37	522.5	92.0	107	3	US-09-982-464-2	Sequence 2, Appli
38	522.5	92.0	107	4	US-10-697-399-2	Sequence 2, Appli
39	522.5	92.0	107	5	US-10-697-400-2	Sequence 2, Appli
40	522.5	92.0	107	5	US-10-911-838-14	Sequence 14, Appl
41	522.5	92.0	107	5	US-10-911-838-21	Sequence 21, Appl
42	522.5	92.0	107	6	US-11-102-403-3	Sequence 3, Appli
43	522.5	92.0	128	4	US-10-478-056-31	Sequence 31, Appl
44	522.5	92.0	139	4	US-10-687-799-55	Sequence 55, Appl
45	522	91.9	106	6	US-11-021-715-99	Sequence 99, Appl

ALIGNMENTS

RESULT 1  
US-09-920-267C-8  
; Sequence 8, Application US/09920267C  
; Publication No. US20030040044A1  
; GENERAL INFORMATION:  
; APPLICANT: Centocor, Inc.  
; APPLICANT: Giles-Komar, Jill  
; APPLICANT: Trikha, Mohit  
; APPLICANT: Snyder, Linda  
; APPLICANT: Nakada, Marian  
; TITLE OF INVENTION: ANTI-DUAL INTEGRIN ANTIBODIES, COMPOSITINS, METHODS AND USES  
; FILE REFERENCE: CEN 249  
; CURRENT APPLICATION NUMBER: US/09/920,267C  
; CURRENT FILING DATE: 2001-08-01  
; PRIOR APPLICATION NUMBER: 60/223,363  
; PRIOR FILING DATE: 2000-08-07  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 8  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-920-267C-8

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Best Local Similarity	99.1%;	Pred. No. 1.8e-41;		
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Qy	61	RFGSGSGTDTLT	ISSLEPEDFAVY	CQQRSNWPPFTFGPGTKVDIK
Db	61	RFGSGSGTDTLT	ISSLEPEDFAVY	CQQRSNWPPFTFGPGTKVDIK

RESULT 2  
US-10-305-347A-8  
; Sequence 8, Application US/10305347A  
; Publication No. US20030143603A1  
; GENERAL INFORMATION:  
; APPLICANT: Giles-Komar, Jill  
; APPLICANT: Bernie Scallon  
; TITLE OF INVENTION: ANTI-TNF ANTIBODIES, COMPOSITIONS, METHODS AND USES  
; FILE REFERENCE: CEN5005  
; CURRENT APPLICATION NUMBER: US/10/305,347A  
; CURRENT FILING DATE: 2002-11-26  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver 3.0



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; SEQ ID NO 8
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-305-347A-8

Query Match          98.4%; Score 559; DB 4; Length 108;
Best Local Similarity 99.1%; Pred. No. 1.8e-41;
Matches 107; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db      1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQOKPGQAPRLLIYDASNRATGIPA 60

Qy      61 RFSGSGSGTDFTLTISLSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
Db      61 RFSGSGSGTDFTLTISLSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108

RESULT 3
US-10-720-323-8
; Sequence 8, Application US/10720323
; Publication No. US20040185507A1
; GENERAL INFORMATION:
; APPLICANT: Centocor, Inc.
; APPLICANT: Giles-Komar, Jill
; APPLICANT: Trikha, Mohit
; APPLICANT: Snyder, Linda
; APPLICANT: Nakada, Marian
; TITLE OF INVENTION: ANTI-DUAL INTEGRIN ANTIBODIES, COMPOSITINS, METHODS AND USES
; FILE REFERENCE: CEN 249 CIPNP
; CURRENT APPLICATION NUMBER: US/10/720,323
; CURRENT FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: 60/223,363
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-720-323-8

Query Match          98.4%; Score 559; DB 4; Length 108;
Best Local Similarity 99.1%; Pred. No. 1.8e-41;
Matches 107; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      61 RFSGSGSGTDFTLTISLSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
Db      61 RFSGSGSGTDFTLTISLSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108

RESULT 4
US-10-954-900A-8
; Sequence 8, Application US/10954900A
; Publication No. US20050123541A1
; GENERAL INFORMATION:
; APPLICANT: Giles-Komar, Jill
; APPLICANT: David Shealy
; APPLICANT: David Knight
; APPLICANT: Bernie Scallon
; APPLICANT: George Heavner
; TITLE OF INVENTION: ANTI-TNF ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN0250 DIV-2
; CURRENT APPLICATION NUMBER: US/10/954,900A
; CURRENT FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: 09/920,262
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/223,360
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; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 60/236,826
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO 8
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-954-900A-8

Query Match          98.4%; Score 559; DB 5; Length 108;
Best Local Similarity 99.1%; Pred. No. 1.8e-41;
Matches 107; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db      1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQOKPGQAPRLLIYDASNRATGIPA 60

Qy      61 RFSGSGSGTDFTLTISLSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
Db      61 RFSGSGSGTDFTLTISLSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108

RESULT 5
US-11-009-731-90
; Sequence 90, Application US/11009731
; Publication No. US20050191293A1
; GENERAL INFORMATION:
; APPLICANT: DESHPANDE, Shirkant
; APPLICANT: HUANG, Haichun
; APPLICANT: SRINIVASAN, Mohan
; APPLICANT: CARDARELLI, Josephine M.
; APPLICANT: WANG, Changyu
; APPLICANT: PASSMORE, David
; APPLICANT: RANGAN, Vangipuram
; APPLICANT: LANE, Thomas E.
; APPLICANT: KEIRSTEAD, Hans S.
; APPLICANT: LIU, Michael T.
; TITLE OF INVENTION: IP-10 ANTIBODIES AND THEIR USES
; FILE REFERENCE: MXI-312
; CURRENT APPLICATION NUMBER: US/11/009,731
; CURRENT FILING DATE: 2004-12-10
; PRIOR APPLICATION NUMBER: 60/529180
; PRIOR FILING DATE: 2003-12-10
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 90
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-009-731-90

Query Match          95.2%; Score 541; DB 6; Length 108;
Best Local Similarity 95.4%; Pred. No. 6.7e-40;
Matches 103; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQOKPGQAPRLLIYDASNRATGIPA 60
Db      1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQOKPGQAPRLLIYDASNRATGIPA 60

Qy      61 RFSGSGSGTDFTLTISLSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
Db      61 RFSGSGSGTDFTLTISLSLEPEDFAVYYCQQRSNWPPYTFGQGTKLEIK 108

RESULT 6
US-10-408-901-24
; Sequence 24, Application US/10408901
; Publication No. US20040023313A1
; GENERAL INFORMATION:
; APPLICANT: Boyle, William
; APPLICANT: Huang, Haichun
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; APPLICANT: Elliot, Robin  
; APPLICANT: Sullivan, John  
; APPLICANT: Medlock, Eugene  
; APPLICANT: Martin, Francis  
; TITLE OF INVENTION: Human Anti-OPGL Neutralizing Antibodies As Selective OPGL Pathway  
; TITLE OF INVENTION: Inhibitors  
; FILE REFERENCE: MBHB 01-1145-A  
; CURRENT APPLICATION NUMBER: US/10/408,901  
; CURRENT FILING DATE: 2003-04-07  
; NUMBER OF SEQ ID NOS: 76  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 24  
; LENGTH: 109  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-408-901-24

Query Match 95.2%; Score 541; DB 4; Length 109;  
Best Local Similarity 95.4%; Pred. No. 6.7e-40;  
Matches 103; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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Qy 61 RFGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108  
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Db 61 RFGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPYTFGQGTKLEIK 108

RESULT 7  
US-10-408-901-48  
; Sequence 48, Application US/10408901  
; Publication No. US20040023313A1  
; GENERAL INFORMATION:  
; APPLICANT: Boyle, William  
; APPLICANT: Huang, Haichun  
; APPLICANT: Elliot, Robin  
; APPLICANT: Sullivan, John  
; APPLICANT: Medlock, Eugene  
; APPLICANT: Martin, Francis  
; TITLE OF INVENTION: Human Anti-OPGL Neutralizing Antibodies As Selective OPGL Pathway  
; TITLE OF INVENTION: Inhibitors  
; FILE REFERENCE: MBHB 01-1145-A  
; CURRENT APPLICATION NUMBER: US/10/408,901  
; CURRENT FILING DATE: 2003-04-07  
; NUMBER OF SEQ ID NOS: 76  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 48  
; LENGTH: 215  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-408-901-48

Query Match 95.2%; Score 541; DB 4; Length 215;  
Best Local Similarity 95.4%; Pred. No. 1.3e-39;  
Matches 103; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60

Qy 61 RFGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108  
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Db 61 RFGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPYTFGQGTKLEIK 108

RESULT 8  
US-10-656-769-12  
; Sequence 12, Application US/10656769  
; Publication No. US20040097712A1  
; GENERAL INFORMATION:  
; APPLICANT: Varnum, Brian

; APPLICANT: Witte, Alison  
; APPLICANT: Vezina, Chris  
; APPLICANT: Wong, Lu Min  
; APPLICANT: Qian, Xueming  
; TITLE OF INVENTION: Therapeutic Human Anti-IL-1R Monoclonal Antibody  
; FILE REFERENCE: 01,1554  
; CURRENT APPLICATION NUMBER: US/10/656,769  
; CURRENT FILING DATE: 2003-09-05  
; NUMBER OF SEQ ID NOS: 79  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 12  
; LENGTH: 128  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-656-769-12

Query Match 95.1%; Score 540; DB 4; Length 128;  
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Matches 104; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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Qy 61 RFGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108  
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Db 81 RFGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPLTFGGKTKEIK 128

RESULT 9  
US-10-394-471B-16  
; Sequence 16, Application US/10394471B  
; Publication No. US20040185047A1  
; GENERAL INFORMATION:  
; APPLICANT: Giles-Komar, Jill; Carton, Jill; Scallon, Bernard J.  
; TITLE OF INVENTION: ANTI-TNF ANTIBODIES, COMPOSITIONS, METHODS AND USES  
; FILE REFERENCE: CEN0202  
; CURRENT APPLICATION NUMBER: US/10/394,471B  
; CURRENT FILING DATE: 2003-03-21  
; PRIOR APPLICATION NUMBER: 60/367,903  
; PRIOR FILING DATE: 2002-03-26  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn Ver 3.1  
; SEQ ID NO 16  
; LENGTH: 130  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-394-471B-16

Query Match 95.1%; Score 540; DB 4; Length 130;  
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Matches 104; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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Db 21 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQQKPGQAPRLLIYDASNRATGIPA 80

Qy 61 RFGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108  
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Db 81 RFGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPLTFGGKTKEIK 128

RESULT 10  
US-10-656-769-38  
; Sequence 38, Application US/10656769  
; Publication No. US20040097712A1  
; GENERAL INFORMATION:  
; APPLICANT: Varnum, Brian  
; APPLICANT: Witte, Alison  
; APPLICANT: Vezina, Chris  
; APPLICANT: Wong, Lu Min  
; APPLICANT: Qian, Xueming  
; TITLE OF INVENTION: Therapeutic Human Anti-IL-1R Monoclonal Antibody



; APPLICANT: Hoffmann-La Roche Inc.  
; TITLE OF INVENTION: Antibodies against insulin-like growth factor I receptor and uses  
; TITLE OF INVENTION: thereof  
; FILE REFERENCE: 21695  
; CURRENT APPLICATION NUMBER: US/10/886,838  
; CURRENT FILING DATE: 2004-07-08  
; PRIOR APPLICATION NUMBER: EP 03015526  
; PRIOR FILING DATE: 2003-07-10  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 4  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-886-838-4

Query Match 94.4%; Score 536; DB 5; Length 108;  
Best Local Similarity 95.4%; Pred. No. 1.8e-39;  
Matches 103; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
  
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Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQOKPGQAPRLLIYDASNRATGIPA 60  
  
QY 61 RFGSGSGTDFTLTISSLEPEDFAVYYCQORSNWPPFTFGPTKVDIK 108  
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Db 61 RFGSGSGTDFTLTISSLEPEDFAVYYCQORSKWPPWTFGGTKVEIK 108

RESULT 15  
US-11-021-715-101  
; Sequence 101, Application US/11021715  
; Publication No. US20050208596A1  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Donald L.  
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO ANTI-PLATELET  
; TITLE OF INVENTION: AUTOANTIBODIES AND INHIBITORS THEREOF  
; FILE REFERENCE: 053893-5050  
; CURRENT APPLICATION NUMBER: US/11/021,715  
; CURRENT FILING DATE: 2004-12-23  
; PRIOR APPLICATION NUMBER: PCT/US03/21304  
; PRIOR FILING DATE: 2003-07-03  
; PRIOR APPLICATION NUMBER: 60/394,352  
; PRIOR FILING DATE: 2002-07-03  
; PRIOR APPLICATION NUMBER: 60/411,694  
; PRIOR FILING DATE: 2002-09-18  
; NUMBER OF SEQ ID NOS: 153  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 101  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-021-715-101

Query Match 94.2%; Score 535; DB 6; Length 108;  
Best Local Similarity 94.4%; Pred. No. 2.2e-39;  
Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
  
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Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQOKPGQAPRLLIYDASNRATGIPA 60  
  
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 28, 2005, 14:04:11 ; Search time 6.92308 Seconds  
(without alignments)  
116.825 Million cell updates/sec

Title: US-09-920-137F-8  
Perfect score: 568  
Sequence: 1 EIVLTQSPATLSLSPGERAT.....QQRSNWPPPTFGPGTKVDIK 108

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 57103 seqs, 7488799 residues

Total number of hits satisfying chosen parameters: 57103

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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5: /cgn2\_6/ptodata/1/pubpaa/US09 NEW PUB.pep: \*  
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7: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep: \*  
8: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	539	94.9	108	7 US-11-093-274-23	Sequence 23, Appl
2	531.5	93.6	129	6 US-10-721-763-19	Sequence 19, Appl
3	530.5	93.4	107	7 US-11-093-274-24	Sequence 24, Appl
4	529	93.1	251	7 US-11-054-515-1049	Sequence 1049, Ap
5	528	93.0	108	7 US-11-093-274-22	Sequence 22, Appl
6	522.5	92.0	128	6 US-10-721-763-31	Sequence 31, Appl
7	520.5	91.6	129	6 US-10-721-763-23	Sequence 23, Appl
8	487.5	85.8	107	7 US-11-040-159-17	Sequence 17, Appl
9	487	85.7	95	7 US-11-054-669-86	Sequence 86, Appl
10	487	85.7	95	7 US-11-084-554-138	Sequence 138, App
11	480	84.5	94	7 US-11-093-274-33	Sequence 33, Appl
12	471	82.9	95	7 US-11-054-669-87	Sequence 87, Appl
13	471	82.9	95	7 US-11-084-554-131	Sequence 131, App
14	463.5	81.6	131	6 US-10-721-763-27	Sequence 27, Appl
15	463	81.5	307	7 US-11-000-463-332	Sequence 332, App
16	463	81.5	312	7 US-11-000-463-334	Sequence 334, App
17	462	81.3	251	7 US-11-054-515-1238	Sequence 1238, Ap
18	460	81.0	384	7 US-11-000-463-804	Sequence 804, App
19	460	81.0	384	7 US-11-000-463-805	Sequence 805, App
20	460	81.0	384	7 US-11-000-463-806	Sequence 806, App
21	460	81.0	384	7 US-11-000-463-807	Sequence 807, App
22	459	80.8	247	7 US-11-056-825-8	Sequence 8, Appli
23	459	80.8	249	7 US-11-056-825-4	Sequence 4, Appli
24	457.5	80.5	246	7 US-11-054-515-1268	Sequence 1268, Ap
25	456.5	80.4	250	7 US-11-054-515-1952	Sequence 1952, Ap

26	449.5	79.1	246	7 US-11-054-515-1264	Sequence 1264, Ap
27	447.5	78.8	251	7 US-11-054-515-1219	Sequence 1219, Ap
28	447	78.7	253	7 US-11-054-515-1499	Sequence 1499, Ap
29	445	78.3	108	7 US-11-064-174-178	Sequence 178, App
30	444	78.2	106	7 US-11-174-186-7	Sequence 7, Appli
31	441.5	77.7	252	7 US-11-054-515-1534	Sequence 1534, Ap
32	439.5	77.4	254	7 US-11-054-515-905	Sequence 905, App
33	435	76.6	95	7 US-11-054-669-84	Sequence 84, Appl
34	435	76.6	95	7 US-11-054-669-85	Sequence 85, Appl
35	435	76.6	95	7 US-11-084-554-127	Sequence 127, App
36	435	76.6	95	7 US-11-084-554-130	Sequence 130, App
37	434	76.4	108	7 US-11-064-174-177	Sequence 177, App
38	433	76.2	249	7 US-11-054-515-1035	Sequence 1035, Ap
39	432	76.1	213	7 US-11-172-320-4	Sequence 4, Appli
40	432	76.1	213	7 US-11-173-969-4	Sequence 4, Appli
41	429.5	75.6	96	7 US-11-054-669-88	Sequence 88, Appl
42	429.5	75.6	96	7 US-11-084-554-135	Sequence 135, App
43	428	75.4	108	7 US-11-064-174-31	Sequence 31, Appl
44	428	75.4	108	7 US-11-064-174-161	Sequence 161, App
45	425.5	74.9	242	7 US-11-054-515-1844	Sequence 1844, Ap

ALIGNMENTS

RESULT 1  
US-11-093-274-23  
; Sequence 23, Application US/11093274  
; Publication No. US20050266008A1  
; GENERAL INFORMATION:  
; APPLICANT: Graziano, Robert  
; APPLICANT: Cardarelli, Josephine M.  
; APPLICANT: Kempe, Thomas  
; APPLICANT: Cutter, Beth  
; APPLICANT: Srinivasan, Mohan  
; TITLE OF INVENTION: IRTA-5 ANTIBODIES AND THEIR USES  
; FILE REFERENCE: 04280/1201101-US1  
; CURRENT APPLICATION NUMBER: US/11/093,274  
; CURRENT FILING DATE: 2005-03-28  
; PRIOR APPLICATION NUMBER: 60/557,741  
; PRIOR FILING DATE: 2004-03-29  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 23  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-093-274-23

Query Match 94.9%; Score 539; DB 7; Length 108;  
Best Local Similarity 95.4%; Pred. No. 4.6e-35;  
Matches 103; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy	1	EIVLTQSPATLSLSPGERATLS	SCRASQSVSYLA	WYQQKPGQAPRLLIYDASNRATGIPA	60
Db	1	EIVLTQSPATLSLSPGERATLS	SCRASQSVSYLA	WYQQKPGQAPRLLIYDASNRATGIPA	60
Qy	61	RFGSGSGTDFTLTITSSLEPEDFAVYYCQQRSNWPPPTFGPGTKVDIK			108
Db	61	RFGSGSGTDFTLTITSSLEPEDFAVYYCQQRNNWPPPTFGGTVKVEIK			108

RESULT 2  
US-10-721-763-19  
; Sequence 19, Application US/10721763  
; Publication No. US20050249729A1  
; GENERAL INFORMATION:  
; APPLICANT: KIRIN BEER KABUSHIKI KAISHA  
; TITLE OF INVENTION: ANTI TRAIL-R ANTIBODY  
; FILE REFERENCE: PH-1573-PCT  
; CURRENT APPLICATION NUMBER: US/10/721,763  
; CURRENT FILING DATE: 2003-11-26  
; PRIOR APPLICATION NUMBER: JP2001-150213

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; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: JP2001-243040
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: JP2001-314489
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-721-763-19

Query Match      93.6%; Score 531.5; DB 6; Length 129;
Best Local Similarity 96.3%; Pred. No. 1.9e-34;
Matches 104; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY      1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
      |||
Db      21 EIVLTQSPATLSLSPGERATLSCRASQSVSFLAWYQQKPGQAPRLLIYDASNRATGIPA 80
      |||

QY      61 RFGSGSGTDFTLTISLSEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
      |||
Db      81 RFGSGSGTDFTLTISLSEPEDFAVYYCQQRSNW-PLTFGPGTKVDIK 127

RESULT 3
US-11-093-274-24
; Sequence 24, Application US/11093274
; Publication No. US20050266008A1
; GENERAL INFORMATION:
; APPLICANT: Graziano, Robert
; APPLICANT: Cardarelli, Josephine M.
; APPLICANT: Kempe, Thomas
; APPLICANT: Cutter, Beth
; APPLICANT: Srinivasan, Mohan
; TITLE OF INVENTION: IRTA-5 ANTIBODIES AND THEIR USES
; FILE REFERENCE: 04280/1201101-US1
; CURRENT APPLICATION NUMBER: US/11/093,274
; CURRENT FILING DATE: 2005-03-28
; PRIOR APPLICATION NUMBER: 2005-03-28
; PRIOR FILING DATE: 2004-03-29
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-093-274-24

Query Match      93.4%; Score 530.5; DB 7; Length 107;
Best Local Similarity 96.3%; Pred. No. 2e-34;
Matches 104; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY      1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
      |||
Db      1 EIVLTQSPATLSLSPGERATLSCRASQSVSFLAWYQQKPGQAPRLLIYDASNRATGIPA 60

QY      61 RFGSGSGTDFTLTISLSEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
      |||
Db      61 RFGSGSGTDFTLTISLSEPEDFAVYYCQQRSNWPP-TFGQGTKVEIK 107

RESULT 4
US-11-054-515-1049
; Sequence 1049, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
```

```

; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1049
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1049

Query Match      93.1%; Score 529; DB 7; Length 251;
Best Local Similarity 95.4%; Pred. No. 5e-34;
Matches 103; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
      |||
Db      143 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQQKPGQAPRLLIYDASNRATGIPA 202
      |||

QY      61 RFGSGSGTDFTLTISLSEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
      |||
Db      203 RFGSGSGTDFTLTISLSEPEDFAVYYCQQRSNWPPFTFGGGTKVEIK 250

RESULT 5
US-11-093-274-22
; Sequence 22, Application US/11093274
; Publication No. US20050266008A1
; GENERAL INFORMATION:
; APPLICANT: Graziano, Robert
; APPLICANT: Cardarelli, Josephine M.
; APPLICANT: Kempe, Thomas
; APPLICANT: Cutter, Beth
; APPLICANT: Srinivasan, Mohan
; TITLE OF INVENTION: IRTA-5 ANTIBODIES AND THEIR USES
; FILE REFERENCE: 04280/1201101-US1
; CURRENT APPLICATION NUMBER: US/11/093,274
; CURRENT FILING DATE: 2005-03-28
; PRIOR APPLICATION NUMBER: 60/557,741
; PRIOR FILING DATE: 2004-03-29
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-093-274-22

Query Match      93.0%; Score 528; DB 7; Length 108;
Best Local Similarity 92.6%; Pred. No. 3.1e-34;
Matches 100; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY      1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
      |||
Db      1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
      |||
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Query Match 85.7%; Score 487; DB 7; Length 95;  
Best Local Similarity 98.9%;  
Pred. NO. 3.4e-31;  
Matches 94; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

<b>Qy</b>	1 EIVLTQSPATLSLSPGERATLSCRASQSVSYSIAYWYQQKPGQAPRLIIYDASNRATGIPA 60 
<b>D<sub>b</sub></b>	1 EIVLTQSPATLSLSPGERATLSCRASQSVSYSIAYWYQQKPGQAPRLIIYDASNRATGIPA 60 

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RESULT 10
US-11-084-554-138
; Sequence 138, Application US/11084554
; Publication No. US20050260679A1
; GENERAL INFORMATION:
; APPLICANT: Kellermann, Sirid-Ai
; APPLICANT: Green, Larry L.
; APPLICANT: Korver, Wouter
; TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
; TITLE OF INVENTION: ANTIBODIES THROUGH V GENE MANIPULATION
; FILE REFERENCE: ABGENIX.100A
; CURRENT APPLICATION NUMBER: US/11/084,554
; CURRENT FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: 60/554,372
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: 60/574,661
; PRIOR FILING DATE: 2004-05-24
; NUMBER OF SEQ ID NOS: 266
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 138
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-084-554-138

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```
Query Match      85.7%; Score 487; DB 7; Length 95;
Best Local Similarity 98.9%;
Pred. No. 3.4e-31;
Matches 94; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQQKPGQAPRLIIYDASNRATGIPA 60

Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQQKPGQAPRLIIYDASNRATGIPA 60

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RESULT 11
US-11-093-274-33
; Sequence 33, Application US/11093274
; Publication No. US20050266008A1
; GENERAL INFORMATION:
; APPLICANT: Graziano, Robert
; APPLICANT: Cardarelli, Josephine M.
; APPLICANT: Kempe, Thomas
; APPLICANT: Cutter, Beth
; APPLICANT: Srinivasan, Mohan
; TITLE OF INVENTION: IRTA-5 ANTIBODIES AND THEIR USES
; FILE REFERENCE: 04280/1201101-US1
; CURRENT APPLICATION NUMBER: US/11/093,274
; CURRENT FILING DATE: 2005-03-28
; PRIOR APPLICATION NUMBER: 60/557,741
; PRIOR FILING DATE: 2004-03-29
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 33
; LENGTH: 94
; TYPE: PRT
; ORGANISM: Homo sapiens

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US-11-093-274-33

Query Match	84.5%;	Score 480;	DB 7;	Length 94;
Best Local Similarity	98.9%;	Pred. No. 1.1e-30;		
Matches 93: Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

Qy	1	EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQQKPGQAPRLLIYDASN	60
Qy	1	EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQQKPGQAPRLLIYDASN <td>60</td>	60
Db	1	EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQQKPGQAPRLLIYDASN <td>60</td>	60
Qy	61	RFSGSGSGTDFTLTITISLSEPEDFAVYYCQQRSNW	94
Db	61	RFSGSGSGTDFTLTITISLSEPEDFAVYYCQQRSNW	94

RESULT 12  
US-11-054-669-87  
; Sequence 87, Application US/11054669  
; Publication No. US20050261480A1  
; GENERAL INFORMATION:  
; APPLICANT: Foote, Jefferson  
; TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES  
; FILE REFERENCE: 30219/US/3  
; CURRENT APPLICATION NUMBER: US/11/054,669  
; CURRENT FILING DATE: 2005-02-08  
; PRIOR APPLICATION NUMBER: US 10/194,975  
; PRIOR FILING DATE: 2002-07-12  
; PRIOR APPLICATION NUMBER: US 60/305,111  
; PRIOR FILING DATE: 2001-07-12  
; NUMBER OF SEQ ID NOS: 124  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 87  
; LENGTH: 95  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-11-054-669-87

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Query Match      82.9%; Score 471; DB 7; Length 95;
Best Local Similarity 96.8%; Pred. No. 5.5e-30;
Matches 91; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Qy	1	EIVLTQSPATLSLSPGERATLSRASQSIVSYLAWYQQKPGQAPRLIIYDASNRATGIPA	60
Dd	1	EIVLTQSPATLSLSPGERATLSRASGVSSYLAWYQQKPGQAPRLIIYDASNRATGIPA	60
Qy	61	RFGSGSGTDFTLTISILEPEDFAVYYCOORSNW	94
Dd	61	RFGSGSGTDFTLTISILEPEDFAVYYCOORSNW	94

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RESULT 13
US-11-084-554-131
; Sequence 131, Application US/11084554
; Publication No. US20050260679A1
; GENERAL INFORMATION:
; APPLICANT: Kellermann, Sirid-Ai
; APPLICANT: Green, Larry L.
; APPLICANT: Korver, Wouter
; TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
; TITLE OF INVENTION: ANTIBODIES THROUGH V GENE MANIPULATION
; FILE REFERENCE: ABGENIX.100A
; CURRENT APPLICATION NUMBER: US/11/084,554
; CURRENT FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: 60/554,372
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: 60/574,661
; PRIOR FILING DATE: 2004-05-24
; NUMBER OF SEQ ID NOS: 266
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 131
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens

```

•



```
US-11-084-554-131
Query Match      82.9%; Score 471; DB 7; Length 95;
Best Local Similarity 96.8%; Pred. No. 5.5e-30;
Matches 91; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 EIVLTQSPATLSLSPGERATLSCRASQSVSYSLAWYQQKPGQAPRLIIYDASNRATGIPA 60
      |||
Db      1 EIVLTQSPATLSLSPGERATLSCRASQSVSYSLAWYQQKPGQAPRLIIYDASNRATGIPA 60

Qy      61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNW 94
      |||
Db      61 RFSGSGPGTDFTLTISSLEPEDFAVYYCQQRSNW 94

RESULT 14
US-10-721-763-27
; Sequence 27, Application US/10721763
; Publication No. US20050249729A1
; GENERAL INFORMATION:
; APPLICANT: KIRIN BEER KABUSHIKI KAISHA
; TITLE OF INVENTION: ANTI TRAIL-R ANTIBODY
; FILE REFERENCE: PH-1573-PCT
; CURRENT APPLICATION NUMBER: US/10/721,763
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: JP2001-150213
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: JP2001-243040
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: JP2001-314489
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-721-763-27

Query Match      81.6%; Score 463.5; DB 6; Length 131;
Best Local Similarity 85.3%; Pred. No. 2.6e-29;
Matches 93; Conservative 5; Mismatches 10; Indels 1; Gaps 1;

Qy      1 EIVLTQSPATLSLSPGERATLSCRASQSV-YSYLAWYQQKPGQAPRLIIYDASNRATGIP 59
      |||
Db      21 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLIIYGASSRATGIP 80

Qy      60 ARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
      |||
Db      81 DRFSGSGSGTDFTLTISSLEPEDFAVYYCQYGSSPPLYTFGQGTKLEIK 129

RESULT 15
US-11-000-463-332
; Sequence 332, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Drmanac, Radojic T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
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; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 332
; LENGTH: 307
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-000-463-332

Query Match      81.5%; Score 463; DB 7; Length 307;
Best Local Similarity 87.2%; Pred. No. 5.5e-29;
Matches 95; Conservative 2; Mismatches 10; Indels 2; Gaps 2;

Qy      1 EIVLTQSPATLSLSPGERATLSCRASQSV-YSYLAWYQQKPGQAPRLIIYDASNRATGIP 59
      |||
Db      150 EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLIIYGASSRATGIP 209

Qy      60 ARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
      |||
Db      210 DRFSGSGSGTDFTLTISSLEPEDFAVYYCQQTGRIPP-TFGQGTKVEIK 257

Search completed: December 28, 2005, 14:23:18
Job time : 7.92308 secs
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November 2005

Published Applications Nucleic Acid and Published Applications Amino Acid database searches now generate two sets of results each. The Published Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published Applications New databases; older published applications make up the Published Applications Main databases.

Searches run against Nucleic Acid Published Applications produce two sets of results, with the extensions **.rnpbm** (Published Applications\_NA\_Main) and **.rnpbn** (Published Applications\_NA\_New).  
Searches run against Amino Acid Published Applications produce two sets of results, with the extensions **.rapbm** (Published Applications\_AA\_Main) and **.rapbn** (Published Applications\_AA\_New).

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Db      2 VQLVQSGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYYA 61
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QY      62 DSVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCARDR-----GIAAGGNYYYYGMDVWG 117
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      62 DSVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCARDREAYYDILTGYLLYYTMDVWG 121
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      118 QGTTVTVSS 126
      :|||||:
Db      122 RGTVTVSS 130
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RESULT 8
US-11-054-515-1394
; Sequence 1394, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLYs
```

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; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1394
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1394
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Query Match      82.4%; Score 550.5; DB 7; Length 252;
Best Local Similarity 82.2%; Pred. No. 3.9e-40;
Matches 106; Conservative 7; Mismatches 13; Indels 3; Gaps 1;
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QY      1 QVQLVESGGGVQPGRSLRLSCAASGFI FSSYAMHWVRQAPGNGLEWVAFMSYDGSNKYY 60
      :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      1 EVQLVQSGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY 60
      :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY      61 ADSVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCARDRG---IAAGGNYYYYGMDVWG 117
      :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      61 ADSVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAKEESYYDILTGYVVHYGMDVWG 120
      :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY      118 QGTTVTVSS 126
      :|||:||||
Db      121 KGT LVTVSS 129
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```
RESULT 9
US-11-054-515-981
; Sequence 981, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
```

```
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLYs
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 981
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-981
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Query Match      82.2%; Score 549; DB 7; Length 254;
Best Local Similarity 84.4%; Pred. No. 5.3e-40;
Matches 108; Conservative 4; Mismatches 14; Indels 2; Gaps 1;

QY      1 QVQLVESGGGVQPGRSLRLSCAASGFI FSSYAMHWVRQAPGNGLEWVAFMSYDGSNKYY 60
      :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      1 QVQLVQSGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY 60
      :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY      61 ADSVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCARDRGI--AAGNYYYYYGM DVMGQ 118
      :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      61 ADSVKGRFTISRDN SKNTLYLQMN SLRAGDTAVYYCARDRGYYDILTGYRGHGMDVMGR 120
      :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY      119 GTT VTVSS 126
      |||:||||
Db      121 GTL VTVSS 128
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```
RESULT 10
US-11-064-174-140
; Sequence 140, Application US/11064174
; Publication No. US20050282252A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/11/064,174
; CURRENT FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US/09/240,274
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/081,380
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 140
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
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```

; OTHER INFORMATION: anti-Rh(D) antibody clone SH16
US-11-064-174-140

Query Match      82.1%; Score 548.5; DB 7; Length 125;
Best Local Similarity 83.3%; Pred. No. 3e-40;
Matches 105; Conservative 9; Mismatches 11; Indels 1; Gaps 1;

QY      1 QVQLVESGGGVVQPGRSLRLSCAASGFIFFSSYAMHWVRQAPGNGLEWVAFMYSYDGSNKKY 60
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Db      1 EVQLLESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGRGLEWVALIWDGGENKEY 60

QY      61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDRGIAAGGNYYYYYGMVDVWGQGT 120
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Db      61 ADSVKGRFSISRDNKNTLYLQVNSLRADDTAVYYCARDQR-AAAGIFYYSRMDVWGQGT 119

QY      121 TTVTVSS 126
      |||||
Db      120 TTVTVSS 125

RESULT 11
US-11-084-554-8
; Sequence 8, Application US/11084554
; Publication No. US20050260679A1
; GENERAL INFORMATION:
; APPLICANT: Kellermann, Sirid-Ai
; APPLICANT: Green, Larry L.
; APPLICANT: Korver, Wouter
; TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
; TITLE OF INVENTION: ANTIBODIES THROUGH V GENE MANIPULATION
; FILE REFERENCE: ABGENIX.100A
; CURRENT APPLICATION NUMBER: US/11/084,554
; CURRENT FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: 60/554,372
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: 60/574,661
; PRIOR FILING DATE: 2004-05-24
; NUMBER OF SEQ ID NOS: 266
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-084-554-8

Query Match      82.0%; Score 547.5; DB 7; Length 125;
Best Local Similarity 86.5%; Pred. No. 3.6e-40;
Matches 109; Conservative 3; Mismatches 13; Indels 1; Gaps 1;

QY      1 QVQLVESGGGVVQPGRSLRLSCAASGFIFFSSYAMHWVRQAPGNGLEWVAFMYSYDGSNKKY 60
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWAVIWSDSIKYY 60

QY      61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDRGIAAGGNYYYYYGMVDVWGQGT 120
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAREVESAMGG-FYINGMDVWGQGT 119

QY      121 TTVTVSS 126
      |||||
Db      120 TTVTVSS 125

RESULT 12
US-11-054-515-397
; Sequence 397, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
```

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; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 397
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-397

Query Match      81.7%; Score 546; DB 7; Length 249;
Best Local Similarity 84.1%; Pred. No. 9.2e-40;
Matches 106; Conservative 3; Mismatches 17; Indels 0; Gaps 0;

QY      1 QVQLVESGGGVVQPGRSLRLSCAASGFIFFSSYAMHWVRQAPGNGLEWVAFMYSYDGSNKKY 60
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 EVNLRESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKKY 60

QY      61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARDRGIAAGGNYYYYYGMVDVWGQGT 120
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKGGYDILTGYSYGYMDVWGQGT 120

QY      121 TTVTVSS 126
      |||||
Db      121 MVTVSS 126

RESULT 13
US-11-054-515-1102
; Sequence 1102, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
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# WEST Search History

Hide Items | Restore | Clear | Cancel

DATE: Friday, January 06, 2006

Hide? Set Name Query Hit Count

DB=USPT; PLUR=YES; OP=OR

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<input type="checkbox"/>	L1	anti adj Tnf adj antibody	338
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END OF SEARCH HISTORY



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175117

**STIC-Biotech/ChemLib**

**From:** Seharaseyon, Jegatheesan  
**Sent:** Tuesday, December 27, 2005 3:25 PM  
**To:** STIC-Biotech/ChemLib  
**Subject:** Re:09/920137

**Importance:** High

VRF E

Hi,

Please search SEQ ID NO: 7 and 8 of 09/920137 in both the commercial and interference databases.

Thanks in advance,  
Seyon.

J. Seharaseyon  
Art Unit 1647  
Remsen 4C61  
Mailbox 4C70  
Phone: (571)-272-0892  
Fax: (571)-273-0892

\*\*\*\*\*

Searcher: \_\_\_\_\_  
Searcher Phone: \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date completed: \_\_\_\_\_  
Searcher Prep Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

Type of Search  
NA# \_\_\_\_\_ AA# \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure #: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
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WWW/Internet: \_\_\_\_\_  
Other (Specify): \_\_\_\_\_

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